Sequence:

Run on:

Database

Result

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AV054690 AV054690
AV071084 AV071084
BB357868 BB357868
BG942699 ax28e01.x
A134228 LB56212.x
AV288772 AV288772
AV288772 AV285178
AV285178 AV285178
A1156924 UT-R-C2p-
D60959 HUM143A068
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AV338005 AV336005
B25087 F24122TR IG
A1563911 tn31c07.x
AQ278688 C1TB1-E1-
BE256288 144014 MA
BE236293 144020 MA
                                                                                                                                                                                                                                                                                                      AZ925237 88 bp DNA GSS 01-APR-2001
4910.ez32k18.s1 Saccharomyces paradoxus N17 Saccharomyces paradoxus
AZ925237
                                                                                                                                                                                                                                                                                                                                                                             Eukaryofus, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 88)

1 (bases 1 to 88)

W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
Unpublished (2001)
                                                                                                                                                                        BB512144 BB512144
BB256670 BB256670
BI220740 602938853
        AZ818519 3
AQ985182 1
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BB512144
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BI293223
BB171532
BB310621
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BB503511
BB510596
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/db_xref="taxon:27291"
/clone="4910.ez32k18.31"
/clone_lib="Saccharomyces paradoxus N17"
/note="Random genomic sequence "
R q 42 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, 1
Tel: 314 362 2735
Fax: 314 362 7855
Email: mj@genetics.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Saccharomyces paradoxus"
/strain="N17"
                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: random plasmid subclone.
Location/Qualifiers
                              AV054690
AV071084
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AI345298
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RESULT 1
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AA579315 nf36e06.s
AU180504 AU180504
AQ009485 CIT-HSP-2
AV333933 AV333933
BF881282 QV1-ET018
BF891282 QV1-ET018
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AZ289196 RPCI-23-5
AI610647 tp20d02.x
BE145737 IL5-HT020
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                                                            (without alignments)
60.819 Million cell updates/sec
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                                                    3, 2002, 03:52:00 ; Search time 2120.21 Seconds
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Compugen Ltd.
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        GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BE145737
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Maximum DB seq length: 200000000
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zn91e04.s UI-R-DK0-BB171532

AV252038

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AZ289196.1 GI:9530982
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van der Heeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue
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RPCI-23-59823.TJB RPCI-23 Mus musculus genomic clone RPCI-23-59B23,
AZ289196
                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="buds 8mm-to-preanthesis"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; Supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                          Gaps
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/cultivar="TA496"
/cultivar="TA496"
/clone="cTOC6E5"
/clone="TOC6E5"
/clone_lb="tomato flower buds 8 mm to pre-anthesis,
                                                                                                                                                                                                                                                     AW217731 118 bp mRNA EST 18-WAY-200
EST296445 tomato flower buds 8 mm to pre-anthesis, Cornell
University Lycopersicon esculentum cDNA clone cTGC6E5, mRNA
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                  Length 88;
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                                                  Ouery Match 100.0%; Score 12; DB 13; Best Local Similarity 100.0%; Pred. No. 7.3e+03; Matches 12; Conservative 0; Mismatches 0;
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1. .118
                                                                                                                                                                                                                                                                                                                           AW217731
AW217731.1 GI:6528605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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Matches 12; Conserv
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AW217731/c
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CooRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

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                                                                                                                              Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 59 row: B column: 23
Seq primer: SP6
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 126)
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42D6402.x1 NCI_CGAP_GASA Homo sapiens CDNA clone IMAGE:2188323 3'
similar to SW:ULCE_HCMVA PI6835 HYPOTHETICAL PROTEIN UL126.
;contains element LTRS repetitive element; ', mRNA sequence.
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                                                                                                                                                                                                                        Mouse BAC End Sequences from Library RPCI-23 (Dpublished (1999) Contact: Shaying Jabo Contact: Shaying Jabo Department of Eukaryotic Genomics The Institute for Genomic Research 7712 Medical Center Dr., Rockville, MD 20850, USA 791: 301 838 0208
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100.0%; Pred. No. 7.1e+03;
tive 0; Mismatches 0;
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/clone_lib="RPCI-23"
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/lab_host="DH10B"
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Mus musculus
Eukaryota; Metazoa;
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/organism="Homo sapiens"
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/db_xref="taxon:966"
/clone_lib="Hr0207"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A min1-library was made by cloning products
Site_2: SmaI; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL5-HT0207-231 (999-006-A01&t3=1999-10-23&t4=1) Seq primer: puc 18 forward High quality sequence start: 56 High quality sequence start: 56 High quality sequence stop: 147.
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1 (bases 1 to 147)

1 (bases 1 to 147)

2 (bases 1 to 147)

3 (bubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K. Global analysis of gene expression in colon mucosa: a large scale random cDNA sequencing analysis

Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K. Institute for Molecular and Cellular Biology

Osaka University, Osaka 565, Japan.

Location/Qualifiers
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26 t
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/note="Adult male, tissue_type =
24 c 34 g 26 t
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/db_xref="taxon:9606"
/clone="cm1984"
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                  Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Ste_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
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IL5-HT0207-231099-006-A01 HT0207 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147)
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/db_xref="taxon:9606"
/clone="InAGE:1488323"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring call features"
/lab_host="DH108"
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Seg primer: -40UP from Gibco
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RESULT 7 AA579315/c DEFINITION

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AQ009485 155 bp DNA GSS 27-JUN-1998
CIT-HSP-22283N16.TRB CIT-HSP Homo sapiens genomic clone 2283N16, DNA
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Sanaka, E., Hori H., Naruse, K., Mitani, H. and Tanaka, M. Medaka EST analysis
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 155)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K. Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
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Seg primer: MI3 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="aduit"
/note="Wild samples from Okayama Pref.(Southern part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryzias latipes"
/strain="wild type"
/db_xref="taxon:8090"
/clone="NGT10.02c"
/clone=lib="Medaka eye cDNA library (SNK01)"
/tissue_type="eye"
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Other GSSs: CIT-HSP-2283NI6.TFB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                      Graduate School of Science, Nagoya University
Furo-Cho, Chikusa-ku, Nagoya 464-8602, Japan
Faz: 81-52-789-2974
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iive 0; Mismatches 0;
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Contact: Emi Sanaka
Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: Gapdbs-refmail.nih.gov
Email: Gapdbs-refmail.nih.gov
Tissue Procurement: W. Marcha Linehan, M.D., Rodrigo Chuaqui, M.D.,
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Content distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.linl.gov/bbrp/image/image.html
Insert Length: 578 Std Error: 0.00
Seq primar: -40m13 fwd. Er from Amersham
High quality sequence stop: 126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pawp10; site_1: Not1; site_2: EcoR1; lst strand cDNA was primed with oligo(dT)17 on 50 ng of DNAs-treated, total cellular RNA obtained from 5,000-10,000 microdisseted preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoR1 adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pawP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
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AU180504 Medaka eye CDNA library (SNKOl) Oryzias latipes CDNA clone
NGY10 02c, mRNA sequence.
AU180504.1 GI:13429341
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                                             AA579315 150 bp mRNA EST 12-SEP-1997 nf36e06.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:915874, mRNA
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                 AA579315.1 GI:2357499
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/tissue_type="medulla oblongata"
/dev_stage="adult"
/lab_host="DH10B"
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    .165
    /organism="Mus musculus"

                                                                                                                /db_xref="taxon:10090"
/clone="6330552F17"
                        Location/Qualifiers
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                                                                                             /strain="C57BL/6J
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BF881282
BF881282.1 GI:12271408
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (basea 1 to 165)

8. Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Eukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
15hi, Y., Ishikawa, T., Itoh, M., Izawa, M., Radota, K., Ragawa, I., Kai,
15hi, Y., Ishikawa, T., Itoh, M., Izawa, M., Oda, R., Odazaki, Y.,
Matsuyama, T., Miki, R., Mizuno, Y., Koya, S., Kusakabe, M., Oda, H., Okazaki, Y.,
Nayo, J., Shiraki, T., Sano, M., Sato, K., Shibata, Y., Shipata, Y., Shipama, T., Watahiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Konno, H., et al. 1999)

NL Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itch, M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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M.E.http://genome-gsc.riken.go.jp,
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV333933 RIKEN Full-length enriched, adult male medulla oblongata Mas musculus cDNA clone 6330552F17 3' similar to X04070 Rat liver mRNA for gap junction protein, mRNA sequence.
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999).
Carninci,P. and Hayashizaki'y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                            /sex="Male"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
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                        1. .155
/organism≂"Homo sapiens"
                                                                  /db_xref="GDB:7148131"
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Location/Qualifiers
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FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and /clone_lib="RIKEN full-length enriched, adult male medulla oblongata" ö Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed Gaps BF881282 165 bp mRNA EST 17-JAN-2001 QVI-ET0183-021200-529-d05_1 ET0183 Homo sapiens cDNA, mRNA ; 0 Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 100.0%; Score 12; DB 10; Length 165; 100.0%; Pred. No. 7e+03; ive 0; Mismatches 0; Indels

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Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                         /note="Organ: lung_tumor; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of Lissue mRNA and cDNA amplification were performed under lissue mRNA and conditions."
           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-ET0183-021200-529-d05_1&t3=2000-12-02&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 165.
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1 (bases 1 to 171)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-UT0058-
181000-007-901&t5=2000-10-18&t4=1)
Seq primer: puc 18 forward
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PM3-UT0058-181000-007-901 UT0058 Homo sapiens CDNA, mRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0183"
/dev_stage="Adult"
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High quality sequence stop: 113
Location/qualifiers
1..171
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100.0%;
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BF909645.1 GI:12301103
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oy. ga E

COMMENT

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/note="Organ: uterus_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196,716 - Individ Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Liver library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. consortium at LLNL (info@image.llnl.gov). IMAGE ID=1782730
FOLYA=NO.
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/clone_lib="UI-R-CO"
/clone_lib="UI-R-CO"
/dev_stage="adult"
/lab_host="DHJDB [Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-Al
and UI-R-El libraries. The UI-R-Al library consisted of a
mixture of individually tagged normalized libraries
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451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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    .172
    /organism="Rattus norvegicus"

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42 c 49 g 46 t
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/db_xref="taxon:9606"
                                    /clone_lib="UT0058"
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AQ985182/c
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constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified CDNA inserts from a pool of UI-R-AI and UI-R-EI clones from which is seried as a driver in a hybridization with the pooled UI-R-AI and UI-R-EI library in the form of single-stranded circles. The remaining single-stranded circles. The remaining single-stranded circles and electroporated to doubble-stranded circles and electroporated to bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described 18pnaldo, Lennon and Soares, Genome Research 6: 791-806,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2M0088A10R Mouse 10kb plasmid UUCC1M library Mus musculus genomic clone UUGC2M008BA10 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 184112, USA
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/db_xref="taxon:10090"
/db_xref="taxon:0090"
/clone="lib="Mouse 10kb plasmid UUGCIM library"
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Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: A column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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Fax: 801 585 7177
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TITLE

SOURCE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114 |qb|AR123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll xL10-Gold (Stratagene) cells and selected for ampleillin resistance."
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Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RFCI-23-307MS.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: szhaottygr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library and albulity, please contact Pieter de Jong
(pieter@dejong.med.bulfalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bulfalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 307 row: M column: 5
Seq primer: SP6
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RPCI-23-307M5.TJ RPCI-23 Mus musculus genomic clone RPCI-23-307M5,
DNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 177)
/lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /note="Weetcr: PWD42hv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"/strain="C57BL/6J"
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AQ985182.1 GI:6818387
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/db_xref="taxon:10090"
/clone="RPCI-23-307M5"
/clone="lb="RPCI-23"
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/lab_host="Drgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6; mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
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Search completed: April 3, 2002, 04:39:12 Job time: 2832 sec

; 0

Gaps

; 0

Query Match
100.0%; Score 12; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0

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12
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13
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AA291731 ECT296445
AZ289196 RPCI-23-5
AI610647 tp20d02.x
BE145737 IL5-HT020
D25785 HUMGS04153
AA579315 nf36e06.s
AA579315 nf36e06.s
AV33333 AV33333 AV333933
BPB81282 QVI-HSP-2
AV33333 AV333933
                                                               April 3, 2002, 03:52:00; Search time 2120.21 Seconds (without alignments) 60.819 Million cell updates/sec
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                                                                                                                                                                                                                 22703874
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                         11351937 seqs, 5372889281 residues
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                             OM nucleic - nucleic search, using sw model
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AU180504
AQ009485
AV333933
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BF909645
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D25785
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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A1029683 UI-R-CO-1 A2816519 2M0088A10 AQ965182 PRCI-23-3 BF235518 6D2025332 AV054690 AV054690 AV071084 AV071084 BB357868 BB357868 BG342699 ax28e01.x A1345299 tb68c12.x F29452 HSPD19337 H AV288772 AV28772 AV285178 AV285178 A136929 UI-R-C2P- D60559 HUM14AA66B A1572468 tp23401.x AV285178 T24c2P- D60559 HUM14AA66B A1572468 tp23401.x AV285037 F24L22R-IS- BE25629 144014 MA BE25629 HAV14 MA BE25629 144014 MA BE25629 144014 MA BB256670 BB512144 BB512144 BB256670 BB512144 BB152628 HAV014 MA BB23629 11-R-DK0- BB17532 BB171532 BB171532 BB171532 BB17532 BB17532 BB17532 BB17532 BB17532 BB17532 BB505511 BB503511	GSS 01-APR-2001 Ses paradoxus N17 Saccharomyces paradoxus Si, DNA sequence. a: Saccharomycotina; Saccharomycetes; mycetaceae; Saccharomyces. Fulton, L., Graves, T., Miner, T., Gish Johnston, M. nomes to identify functional elements by alysis al School St. Louis, MO 63110, USA au somyces paradoxus" 1291" 118.51" 118.51"
AT029683 AZ818519 AZ818518 AV054690 AV071084 BB357868 BC942699 BC942699 BC942699 BC942699 BC942699 AV28452 AV28452 AV28452 AV28452 AV28452 AV28452 AV28452 AV28452 AV2852 BC959 AV25093 BC9593	Silva
11110000000000000000000000000000000000	18 bp 10.ez132 13.acchar 13.acchar 13.acchar 13.acchar 13.acchar 13.acchar 13.acchar 13.acchar 13.acchar 14.acchar 15.acchar 16.acchar 17.acchar 18.acchar 19.acchar 19.acchar 19.acchar 10.ac
173 173 174 188 188 188 198 198 198 198 198 198 198	ALIGN A2925237 B8 bp DNA 4910.e232x18.s1 Saccharomyces genomic clone 4910.e232x18.s1 A2925237 A2025237 A202527 A
	A2925237 4910.e232k18 genomic clon AZ925237 AZ925237 AZ925237 GSS. Saccharomyce Bukaryota; Bukaryota; P. F. Contact: Joh C
	2522 200.62 2522 2522 2522 2522 2522 2522 2522 2
	AAZ9 AAZ9 AAZ9 AAZ9 AAZ9 AAZ9 AAZ9 AAZ9
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AZ925237/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT FEATURES SOURCE

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Query Match
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1 (bases i to 118)

1 (bases i to 118)
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RPCI-23-59B23.TJB RPCI-23 Mus musculus genomic clone RPCI-23-59B23,
DNA sequence.
AZ289196
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/dev_stage="buds 8mm.to-preanthesis"
/dev_stage="buds 8mm.to-preanthesis"
/note="vector: pBlueScript SK(-): Site_1: EcoR1; Site_2:
Xho1: "upplier: Tanksley: Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size separated while remaining frozen."
                                                                                             Gaps
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Cornell University"
                                                                                                                                                                                                                                                                AW217731 118 bp mRNA EST 18-WAY-200
EST296445 tomato flower buds 8 mm to pre-anthesis, Cornell
University Lycopersicon esculentum cDNA clone cTOC6E5, mRNA
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Email: http://www.genome.clemson.edu/orders/index.html
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                                                      Length 88;
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/cultivar-"TA496"
/db xref="taxon:4081"
/clone-"cTOC6E5"
                                                  Score 12; DB 13;
Pred. No. 7.3e+03;
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                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                                                                                                                          AW217731.1 GI:6528605
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Matches 12; Conservative
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/note="forgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
CooRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderlingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/Dac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 126)
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NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1610647 130 bp mRNA EST 21-APR-1999 tp20d02.xl NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188323 similar to SW:ULC6_HCMVA P16836 HYPOTHETICAL PROTEIN ULl26. contains element LTR5 repetitive element; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                  Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, 1912 B18 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                    Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 12; DB 13; 100.0%; Pred. No. 7.1e+03;
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/clone="RPCI-23-59B23"
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/sex="Female"
/lab_host="DH10B"
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AI610647.1 GI:4619814
AZ289196.1 GI:9530982
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Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-GSP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Dias Neto, E. Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., ds Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE145737 147 bp mRNA EST ZI-JUN-ZUUU
IL5-HT0207-231099-006-A01 HT0207 Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2188323"
/clone_lib=NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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20202663
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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100.0%; Pred. No. 7.1e+03;
iive 0; Mismatches 0;
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High quality sequence stop: 1.
Location/Qualifiers
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="HT0207"
/dev_stage="Adult"
/dot_stage="Adult"
/note="Organ: head_neck; Vertor: pucl8; Site_l: Smal;
Site_l: Smal; A minl-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
31 a 35 c 12 g 69 t.
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-IL5-HT0207-231 099-006-ADIRE3-1999-10-23&t4-1)  
Seq primer: puc 18 forward  
High quality sequence start: 56  
High quality sequence stop: 147.
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Okubo,K., Yoshii,J., Yokouchi,H., Kameyama,M. and Matsubara,K.
Global analysis of gene expression in colon mucosa: a large scale random cDNA sequencing analysis
Compublished (194)
Contact: Okubo,K., Itoh,K., Yoshii,J., Yokouchi,H. and Matsubara,K.
Institute for Molecular and Cellular Biology
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HUMGS04153 Human colon mucosa Homo sapiens CDNA clone cm1984 3'
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/note="Adult male, tissue_type = colon mucosa
24 c 34 g 26 t
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/organism≕"Homo sapiens"
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/clone="cm1984"
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Sanaka, E., Hori, H., Naruse, K., Mitani, H. and Tanaka, M.
Medaka EST analysis
Medaka EST analysis
Unpublished (2001)
Contact: Emi Sanaka
Department of Biological Sciences
Graduate School of Science, Nagoya University
Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan
Tel: 81-52-789-2973
Fax: 81-52-789-2974
Email: sanaka@bio.nagoya-u.ac.jp
This clone was isolated from Medaka eye cDNA library (SNK01) 5'end.
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
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CIT-HSP-22283N16.TRB CIT-HSP HOMO sapiens genomic clone 2283N16, DNA
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Usteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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Seg primer: M13 Reverse
Class: BAC ends.
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/note="Wild samples from Okayama Pref.(Southern part of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Medaka eye cDNA library (SNK01)"
/tissue_type="eye"
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Other_GSSs: CIT-HSP-2283NI6.TFB
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
7912 Madical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryzias latipes"
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/db_xref="taxon:8090"
/clone="NGY10.02c"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@nail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

Tissue Procurement: W. B., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: N.T.GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image-html
Insert Length: 578 Std Error: 0.00
Seq primer: -40ml3 fwd ET from Amersham
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AU180504 Medaka eye CDNA library (SNK01) Oryzias latipes CDNA clone
NGY10.02c, mRNA sequence.
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                                                   AA579315 150 bp mRNA EST 12-SEP-1997 nf36e06.sl NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:915874, mRNA
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:915874"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="45 years old"
/lab_host="DH10B"
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Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                                 /clone="6330552F17"
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/lab_host="DH10B"
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                                                                                                                                                                                                                     /sex="male"
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Wik.http://genome-gsc.riken.go.jp/
Sasaki, N., Izawa.M., watabiki, M., Ozawa.K., Tanaka,T., Yoneda,Y.,
Marsuura,S., Carninci,P., Muramaisu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV333933 165 bp mRNA EST 11-NOV-1999
AV333933 RIKEN full-length enriched, adult male medulla oblongata uks musculus cDNA clone 6330552F17 3' similar to X04070 Rat liver mRNA for gap junction protein, mKNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                              /organism="Homo sapiens"
                                                               /db_xref="GDB:7148131"
/db_xref="taxon:9606"
/clone="2283N16"
/clone=lib="CIT-HSP"
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  Location/Qualifiers
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                                                                                                                       /clone_lib="RIKEN full-length enriched, adult male medulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGAGAGAGACTCTTTTTTTTTTTTTTVN 3'], cDNA was
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Mammalia; Eutheria; Primates; Calarrhini; Hominidae; Homo.
1 (bases 1 to 165)
                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia
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QV1-ET0183-021200-529-d05_1 ET0183 Homo sapieus cDNA, mRNA
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                                                                                                                                                                                                                    /tissue_type="medulla oblongata"
/organism="Mus musculus"
/strain="C57BL/6J"
                                                             /db_xref="taxon:10090"
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/organism="Homo sapiens"
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1 (Dases 1 to 171)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fel: +55-11-2704922
Fax: +55-11-2707001
Fault: asimpson@ludwig.org.br
Fhis sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
[http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=PM3&t2=PM3-UT0058-
181000-007-901&t3-2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stor: 13.
Location/Qualifiers
       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=QV1&t2-QV1-EF0183-
021200-529-d05_1&t3=2000-12-02&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 165.
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PM3-UT0058-181000-007-901 UT0058 Homo sapiens CDNA, mRNA sequence.
BF909645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 12; DB 11; Length 165; 100.0%; Pred. No. 7e+03;
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Ludwig Institute for Cancer Research
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46 c 35 g 50 t
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                                                                                                                                                                                  /organism="Homo sapiens"
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source

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The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Liver library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1782730
                                                                                    /note="Organ: uterus_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A min!-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under 14 c 49 9 46 t
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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UI-R-CO-iy-b-01-0-UI.S1 UI-R-CO Rattus norvegicus CDNA clone
UI-R-CO-iy-b-01-0-UI 3', mRNA sequence.
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/clone_lib="UI-R-C0"
/dev_stage="adult"
/lab_nost="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996) 97044477
/db_xref="taxon:9606"
/clone_lib="UT0058"
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                                                              /dev_stage="Adult
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100.0%;
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Best Local Similarity 100.
Matches 12; Conservative
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constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified CDNA inserts from a pool of UI-R-AI and UI-R-EI clones from which 3' ESTS had been derived was used as a driver in a hybridization with the pooled UI-R-AI and UI-R-EI library in the form of
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2M0088A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M008BA10 R, DNA sequence.
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Unon, Du, Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                         single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyaparite column chromatography, converted to double-stranded circles and electroporated into DHIUB bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 172;
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Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: A column: 10
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
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FEATURES

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonocleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114) qiblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 177)
Shao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library availability, please contact Pieter de Jong (pieter@deJong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpec.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plater: 307 row: M column: 5 Sea primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ985182 177 bp DNA GSS 30-JAN-2000
PPCI-23-307M5.TJ RPCI-23 Mus musculus genomic clone RPCI-23-307M5,
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Department of Eukaryotic Genomics
The Institute for Genomic Research
The Addical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-307M5.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ985182.1 GI:6818387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 GGATTTTACAGT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ggattttacagt 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence.
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AQ985182/c
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
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/db_xref="taxon:10090"
/clone="RPCI-23-307M5"
/clone="lb="RPCI-23"
/sex="Female"
/sex="Female"
/lab_host="DH10B"
/lab_ho
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'f: Query Match 100.0%; Score 12; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 3, 2002, 04:39:12 Job time: 2832 sec

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ORGANISM: PAG1651UP
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-08-998-416-1071/c
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Sequence 34, Appl
Sequence 34, Appl
Sequence 31, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
                                                                                                               (without alignments)
33.163 Million cell updates/sec
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Sequence 1, Appli
Sequence 6, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6,
Sequence 9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3,
Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14
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Sequence 7
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Sequence 1
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                                                                                              April 3, 2002, 04:09:50; Search time 81.95 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-820-700-7
US-08-343-760A-1
US-08-061-697-34
US-08-113-365B-33
US-08-113-365B-34
US-08-113-365B-34
US-08-668-123-34
US-08-68-123-34
US-08-68-123-34
US-08-67-131-365B-34
US-08-67-13-34
US-08-67-13-34
US-08-470-720-3
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US-09-318-661-6
US-09-230-380-9
US-08-162-475A-3
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US-08-449-043-14
US-08-456-265A-14
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                                                                                                                                                                                                                                                                                351203 seqs, 113238999 residues
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                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-93
                                                                                                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
                                                                                                                                                                                             1 ggattttacagt 12
                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                           US-09-700-187-1
12
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Match Length DB
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                                                                                               Run on:
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117
118
119
122
223
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28 11 91.7 1195 1 US-08-455-416-14 Sequence 14, Appl	29 11 91.7 1195 1 US-08-455-244-14 Sequence 14, App.	-	2 US-08-457-364-14 Sequence 14, i	32 11 91.7 1195 2 US-08-456-262-14 Sequence 14, App	2 US-08-456-240-14 Sequence 14, 1	2 US-08-455-736-14 Sequence 14,		1195 4 US-09-350-600-14 Sequence 14,	1395 1 US-08-806-581A-1 Sequence 1, A	7		m	4 US-09-329-749-9 Sequence 9,	42 11 91.7 1613 1 US-08-219-842-1 Sequence 1, Appl	1 US-08-451-096-1 Sequence 1, i	44 11 91.7 1613 2 US-08-810-599-1 Sequence 1, Appl	45 11 91.7 1622 2 US-09-014-969-16 Sequence 16, App.
28	29	30	31	32	33	34	35	36	c 37	c 38	c 39	40	41	42	43	44	45

ALIGNMENTS

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US-08-999-416-1071/C

US-08-999-416-1071/C

Sequence 1071, Application US/08998416

Patent No. 633954

Remain Promantion

APPLICANT: Poblimain, Rainer

APPLICANT: Poblimain, Rainer

APPLICANT: Remotated, Jurgen

APPLICANT: Mendland, Jurgen

APPLICANT: Remotated, Durgen

APPLICANT: Remotated, Durgen

APPLICANT: Remotated, Philipp

APPLICANT: Remotated, Durgen

APPLICANT: Remotated, Durgen

APPLICANT: Remotated, Philipp

APPLICANT: No. 6339544th Carolina

COUNTRY: USA

ZITP: 27/09

COMPUTER: Remotated, Poology 41sk

COMPUTER: The Compatible

OCMPUTER: Patentin Release #1.0, Version #1.30

COMPUTER: Patentin Release #1.0,

COMPUTER: APPLICATION DATA:

APPLICATION NUMBER: US/08/98,416

FILING DATE: 31-DEC-1997

CLIASSIFICANTION DATA:

APPLICATION NUMBER: APPLICATION HUMBER: PF5-30306/A/CGC1976

FILING DATE: 31-DEC-1996

ATTORNEY APPLICATION NUMBER: PF5-30306/A/CGC1976

FILECOMMUNICATION INFORMATION:

WAME: Weigs, J. Timothy

REGISTRATION PATE: BASE PATE: PF5-30306/A/CGC1976

FILECOMMUNICATION INFORMATION:

TELEFAX: 919-541-6689

SEQUENCE CHARACTERISTICS:

LEMCHARE: DATA (Genomic)

ORIGINAL SYPER: DATA (Genomic)

ORIGINAL SOURCE:

MOLECULE TYPE: DATA (Genomic)

ORIGINALLY SOURCE:

ORIGINAL SOURCE:

ORIGINA
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APPLICANT: Hillman, Jennifer
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
                                                                                                                              E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                           NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                STREET: 3174 Pox
CITY: Palo Alto
STATE: CA
     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LIBRARY: PROSN
; CLONE: 2272281
US-08-903-801-2
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COUNTRY: US
ZIP: 94304
                                                                                                                              ADDRESSEE:
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US-09-295-055-2/c
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                                                     Length 679;
                                                                                                                                                                                                                                                                                                                        APPLICANT: MCCOV, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racio, Lisa A.
APPLICANT: McTory, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                  100.0%; Score 12; DB 4; I
100.0%; Pred. No. 1.1e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12; DB 2;
Pred. No. 1.1e+02;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                 Sequence 5, Application US/08993228
Patent No. 5976838
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: ACCOY, John M.
APPLICANT: LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-903-801-2/c
; Sequence 2, Application US/08903801
; Patent No. 5932712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1138 base pairs
                                                    Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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STRANDEDNESS: double
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                                                                                                                                                236 GGATTTACAGT 225
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985 GGNTTTTACAGT 974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-993-228-5
                                                                                                                          1 ggattttacagt 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U. ZIP: 02140
US-08-998-416-1071
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                                                                                                                                                                                                                                  US-08-993-228-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
APPLICANT: COrley, Noil C.
APPLICANT: Shah, Purvi
APPLICANT: Sha
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OCHUTER: 1BM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastesO for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/903,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Incyte Pharmaceuticals, Inc.: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/09295055
; Patent No. 6232440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1434 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415-855-059
TELEFAX: 415-845-4166
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: PROSNON01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1002 GGATTTTACAGT 991
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                                                                                                                                                                                                                                                                                                                                          Length 2259;
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                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Tissue Differentiation Affecting TITLE OF INVENTION: Factor and Composition NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue STREET: Four Embarcadero Center, Suite 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 12; DB 1; I 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/343,760A
FILING DATE: 22-NOV-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
                                                                                                                                                                                                                                    Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: De Robertis, Edward M APPLICANT: Sasai, Yoshiki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08343760A
Patent No. 5679783
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                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 363-5556
TELEFAX: (415) 362-5418
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3796 base pairs
                                         TELEX: 440706
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
      202-887-0400
                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                       202-835-0605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Four Embarca
CITY: San Francisco
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                    ) ORGANISM: Bacillus;
STRAIN: thompsoni
US-07-828-700-7
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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    TELEPHONE:
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                            TELEFAX:
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APPLICANT: Brown, Kit L.

APPLICANT: Brown, Kit L.

APPLICANT: Whiteley, Helen R.

TITLE OF INVENTION: THORINGIENSIS, GENES ENCODING THEM, AND HOSTS
TITLE OF INVENTION: EXPRESSING THEM
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wegner, Cantor, Mueller & Player
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Wegner, Cantor, Mueller & Player STREET: 1233 20th Street, N.W. CITY: Washington
                     OPERATING SYSTEM: DOS SOFTWARE: COSTWARE: PSASLEDO for Windows Version 2.0 SURRENT APPLICATION DAYs: APPLICATION NUMBER: US/09/295,055
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/903,801
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0354 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,700
FILING DATE: 19920203
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/817,915
FILING DATE: 10 JAN 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/07828700
; Patent No. 5308760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cantor, Herbert I.
REGISTRATION NUMBER: 24,392
REFERENCE/DOCKET NUMBER: P-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1434 base pairs
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: PROSNON01;
CLONE: 2272281
US-09-295-055-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1002 GGATTTTACAGT 991
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                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMEDIATE SOURCE:
                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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US-07-828-700-7
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APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 91.7%; Score 11; DB 1; Length 38; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/131,365B
FILING DATE: 01-OCT-1993
                                         COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,697
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/08131365B Patent No. 5527690 GENERAL INFORMATION:
                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:
TELECOMMUNICATION INFORMATION:
TELEFONE: (512) 320-7200
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic) US-08-061-697-34
                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. Box 4433
CITY: Houston
    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 gattttacagt 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-131-365B-33/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U. ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Brown, Michael S.; Briggs, Michael R.; Wang,
APPLICANT: Xiaodong; Goldstein, Joseph L.
TITLE OF INVENTION: Sterol Regulatory Element Binding Proteins
TITLE OF INVENTION: and Their Use in Screening Assays
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/08051697
Patent No. 5498696
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.; Briggs, Michael R.; Wang,
APPLICANT: Xiaodong; Goldstein, Joseph L.
TITLE OF INVENTION: Sterol Regulatory Element Binding Proteins
TITLE OF INVENTION: and Their Use in Screening Assays
NUMBER OF SEQUENCES:
ADDRESSED: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,697
FILING DATE: CONCURTENTLY Herewith
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100.0%; Pred. No. 3.7e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATOGNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:347/PAR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  STATE: USA
CITY: HOUSTON
CITY: HOUSTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P. O. Box 4433
TATE: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  Sequence 33, Application US/08061697 Patent No. 5498696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (512) 320-7200
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic) US-08-061-697-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.7
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 base pairs
3249 GGATTTTACAGT 3260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                             US-08-061-697-33/c
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UTSD: 372/PAR

TELECOMMUNICATION INFORMATION

TELEPHONE: (512) 418-3000
TELEFRAX: (512) 448-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:

STATE: Texas COUNTRY: USA ZIP: 77210

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Gaps

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APPLICANT: Briggs, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/08668123
Patent No. 5891631
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Briggs, Michael S.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%; Score 11; DB 2; Lk
100.0%; Pred. No. 3.7e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
RECISTRATION NUMBER: 32,165
RECISCOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 418-3000
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,123
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/131,365
FILING DATE: 01-OCT-1993
ATTORNEY AGENT INFORMATION:
NAME: Parker David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                               ; Sequence 33, Application US/08668123; Patent No. 5891631
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                 : P.O. Box 4433
Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                   Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                             US-08-668-123-33/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simmatches 11;
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                                                                                                                                                                                                                                                                                                                                                                        CITY: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%; Score 11; DB 1; La
ilarity 100.0%; Pred. No. 3.7e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                           91.7%; Score 11; DB 1; LA
100.0%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/131,365B
FILING DATE: 01-0CT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                             TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA" US-08-131-3658-33
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08131365B Patent No. 5527690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                           Query Match 91.79
Best Local Similarity 100.0
Matches 11; Conservative
38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 38 base pairs
                        nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 gattttacagt 12
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27 GATTTTACAGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston
STATE: Texas
                      TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-131-365B-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-131-365B-34
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Virginia
COUNTRY: United States
2213: 22313-1404
COMPUTER: REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,720
FILING DATE: 05-JUN 1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Le . 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 003300-293 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/070,455
FILING DATE: 09-JUN-1993
ATTORNEY/AGENT INFORMATION:
  APPLICATION NUMBER: US/07/748,761
                                                                                   GB 9018612.3
                                                                                                                                                                                                                                                                                                                                                                                                    91.7%; Scc.
100.0%; Pre
0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08470720 Patent No. 5824798 GENERAL INFORMATION:
                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9018
FILING DATE: 24-AUG-1990
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
                                                                                                                                          TELEPHONE: (202) 861-3000
TELEFAX: (202) 862-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 836-6620 TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                332 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 base pairs
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 91.7
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                   19910823
                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-07-748-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ggattttacag 11
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                                                                                                                                                                                                                                            LENGTH:
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APPLICANT: Fray, Rupert G
APPLICANT: Lycett, Grantley W
APPLICANT: Brad, Colin R
APPLICANT: Schuch, Wolfgang W
TITLE OF INVENTION: DNA, DNA, DNA, CONStructs, cells and plants
TITLE OF INVENTION: derived therefrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 38;
3.7e+02;
thes 0; Indels
                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby and Cushman
STREET: Eleventh floor, 1615 L Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                         PELICATION NUMBER: US/08/668,123
FILING DATE: 14-JUN-1996
FILING DATE: 14-JUN-1996
FILING DATE: 10-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/131,365
FILING DATE: 01-OCT-1993
ATTORNEY/AGEN: UNCT-1993
NAME: PARKEY, DAVID L.
REGISTRATION NUMBER: 32.165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELEFAX: (512) 414-757
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%; Score 11; DB
100.0%; Pred. No. 3.7
ive 0; Mismatches
            E: Arnold, White & Durkee P.O. Box 4433
                                                                              STATE: Texas
COUNTRY: 0.S.A.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc " DNA"

US-08-668-123-34
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100.0%; Pre
0;
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Patent No. 5304490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.7
Best Local Similarity 100.
Matches 11; Conservative
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 gattttacagt 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Grierso
                                                           Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Wash
STATE: D.C
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US-07-748-761-1/c
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US-09-318-661-3/C
$Sequence 3, Application US/09318661
$ Sequence 3, Application US/09318661
$ Patent No. 6268488
$ GENERAL INFORMATION:
$ APPLICANT: Barbas III, Carlos F.
$ APPLICANT: Barbas III, Carlos F.
$ APPLICANT: Barbas III, Carlos F.
$ APPLICANT: Latt. Benjamin
$ APPLICANT: Lerner, Richard A.
$ TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
$ TITLE REFERENCE: PLF0011S
$ CURRENT FILING DATE: 1999-05-25
$ NUMBER OF SEQ ID NOS: 6
$ SOFTWARE: PATENTIN VET. 2.1
$ SEQ ID NO 3
$ LENGTH: 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: residue sequence of catalytic fragment.
NAME/KEY: CDS
LOCATION: (1)..(855)
is LOCATION: (1)..(855)
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MOLECULE TYPE: DNA (genomic) FEATURE:
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367 GGATTTTACAG 357
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; LOCATION: 1..15
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; LOCATION: 101..21
US-08-470-720-3
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Query Score Match Length DB ID	100.0 3441 8 AB007911 4.3 20785 8 AF138704 3.8 5785 8 PSBLOX12	3.5 326924 2 AC093082 AC09308. 3.5 1350 8 PSA17468 Y17468 3.1 146285 9 AC005083 AC00508.	3.1 16343 3 AMFGENOM 3.1 136098 9 AC006970	3.0 245802 2 AC006279 AC006279 2.9 160788 2 AL592166 AL592166 2.9 166133 2 AL593856 , AL593856	2.9 208684 2 AC072048 AC072048 2.9 205429 2 AC005506 AC005506	2.9 224448 2 PFMALAP4 AL035477 2.9 36977 2 AC092304 AC092204 3 9 16621 3 AC032304 AC092304	2.8 185091 2 ACUZID33 ACUZID33 2.8 14867 3 AEO01398 AEO01398 2.8 1867 8 MTSCAJ23 AJ223323	2.7 158398 2 AC011146 2.7 162445 9 AL158151 2.7 1141 6 AX083744 AX083744	63 2.7 162914 2 AC091925 AC091925 Homo sapi 63 2.7 173349 2 AL596253 AL596253 Homo sapi 62.8 2.7 173349 2 AL596253 AL596253 Homo sapi	2.7 213530 2 AC064363 AC068363	2.7 186431 2 AC022281 AC022281 2.7 193302 2 AC021992 AC021992	2.7 45043 Ar200032 Ar200032 2.6 958 B PEALZLLG M80833 P 2.6 103649 2 Ar445319 Ar4454	2.6 147244 9 AC005969 AC005969	2.0 192001 2 FFMALLISFI ALUGATION FIGURE 2.0 100925 9 AC012627 AC012627 AC012627 AC012630 FFMALLISFI AC012600 FFMALLISFI AC012	2.6 185691 2 AC021553	2.6 235532 9 AC008739 AC008739 Homo 2.6 67970 3 PFMAL1P3 AL031746 Plasn	2.6 137332 8 AP002820 2.6 260341 3 CEY116A8C AL11'	2.6 2426 8 SDU49822 2.6 8622 8 YSCMTCYTOC M975	2.6 36977 2 AC092304 2.6 137889 9 AC073269	2.6 140455 2 AL356793 AL35	ALIGNMENTS			ABUU/911 3441 DP DNA PLN 28-SEP-1999 ON Pisum sativum gene for PRA2, complete cds.			Pisum sativum Eukarvota; Viridiplantae;	core eu	Pisum. [1.4]	identification of a cis-regulatory element involved in phytochrome down-regulated expression of the pee small GTPase gene pra2	E 9929394 to 3441)
Result No.		ი 4 დ ტ	7		c 12		c 10 113 118	19 20 c 21	c 23	c 52 c 52		30	33				. c 39						ABOO7911	DEFINITION	ACCESSION VERSION	KEYWORDS SOURCE	ORGANISM		REFERENCE AUTHORS	TITLE	MEDLINE REFERENCE
GenCore version 4.5 Convright (c) 1993 - 2000 Computer Itd	using sw model	Run on: April 3, 2002, 05:14:06; Search time 1999.71 Seconds (without alignments).		Title: US-09-700-187-3 Perfect score: 2325 Sequence: 1 aagctttaaaaggcaagggaatttttgatcttgacaagaaa 2325	•	Gapop 10.0 , Gapext 1.0	nber of hits satisfying chosen par	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	E E ·	Listing iirst	ÿ	3: 95		dv	: Id-q6 : 6				16: em_fun:* 17: em_hum:*			ed by						em_htg_inv:* em_htg_rod:*	<pre>so: em_ntg_otner:* No. is the number of results predicted by chance to have</pre>	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES

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Nagano,Y.

Direct Submission

Direct Submission

Submitted (07-027-1997) Yukio Nagano, Nagoya Universi School of Bloagricultural Sciences; Chikusa, Nagoya, 464-8601, Japan (E-mail:nagano@agr.nagoya-u.ac.jp, Tel:81-52-789-4168, Fax:81-52-789-4296)

Cocation/Qualifiers

Cocation/Qualifiers

i. 3441

/organism="Pisum sativum"

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Source 1.20785 Location/Qualifiers Source 7.20785 Pisum sativum" Acrania-"Alaska 1240. Acrania-"Alaska 1240. Acrania-"Alaska 1240. Ab_xref-"Exaon: 3880 Join(1212. 2468,281. 3142,3416. 3880) Aproduct-gibberellin c20-catdase" Join(1212. 2468,281. 3142,3416. 3879) Acref-"Converts GA12 to GA19 to GA17 and GA20" Acref-"Converts GA12 to GA19 to GA17 and GA20" Acref-"Converts GA12 to GA19 to GA17 and GA20" Acref-"Converts GA12 to GA19 to GA30 and GA20" Acref-"Converts GA12 to GA19 to GA30 and GA20" Acref-"Gil-GB5711 acred	PSBLOX12 PSBLOX12 PSBLOX12 Py38580.1 Cx78580.1 Cx78680.1
FEATURES SOURCE MRNA CDS	123 SULT BLOX12 CUS
DESTITUTION TO THE PROPERTY OF	KEYWORDS SOURCE Pisum sativum Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnolliophyta; endicotyledons; core eudicots; Spermatophyta; Magnolliophyta; Eukaryota; Vicieae; Papillionoideae; Vicieae; Pisum. REFERENCE I (bases I to 20785) Martin, D. N., Percebsting, W. M., Parks, T. D., Dougherty, W. G., Lange, T., Lewis, M. J., Gaakin, P. and Hedden, P. TITLE Feed-back regulation of glibberellin biosynthesis and gene expression in Pisum sativum L. Planta 200 (2), 159-166 (1996) MEDLINE PREFERENCE 2 (bases I to 20785) Martin, D. N. and Proebsting, W. M. TITLE Pisum sativum glibberellin c20-oxidase, genomic clone Unpublished Martin, D. N. and Proebsting, W. M. TITLE ATTLE Direct Submission JOURNAL Submitted (25-MAR-1999) Horticulture, Oregon State University, ALS. 4017, Corvallis, OR 97331-7304, USA

Wed Apr

э; Э Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 326924)
Waterston, R. H.

COMMENT

* 99513 99612: gap of unknown length * 105969 1160668: contig of 6356 bp in length * 105069 112079; contig of 6011 bp in length * 112080 112179; gap of unknown length * 112180 112179; gap of unknown length * 112181 118280: contig of 6011 bp in length * 118181 12620: contig of 8140 bp in length * 126521 126520; gap of unknown length * 126521 134015; contig of 7495 bp in length * 13416 134115; gap of unknown length * 13416 143412: contig of 9297 bp in length * 143413 143512: contig of 8380 bp in length * 14353 118922: contig of 8380 bp in length * 151993 164752: contig of 12760 bp in length * 151993 164752: contig of 12760 bp in length * 164653 164852: gap of unknown length * 164653 164852: contig of 12760 bp in length	180048: gap of unknown length 202365: contig of 2257 bp in 222405: gap of unknown length 232078: gap of unknown length 232078: gap of unknown length 232304: gap of unknown length 25524: contig of 33186 bp in 25534: gap of unknown length 325470: gap of unknown length 325470: gap of unknown length 326924: contig of 1454 bp in 326504: assembly_name:Contig 18" cote="assembly_name:Contig 21" cote="assembly_name:Contig 22" cote="assembly_name:Contig 22" cote="assembly_name:Contig 25" cote="assembly_name:Contig 25" cote="assembly_name:Contig 25" cote="assembly_name:Contig 25" cote="assembly_name:Contig 25" cote="assembly_name:Contig 25" cote="assembly_name:Contig 29" cote="asse	
University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	11669 345: contig of 1568 bp in length 1669 345: contig of 1675 bp in length 3466 4925 contig of 1675 bp in length 4926 5925: contig of 1675 bp in length 4926 5925: contig of 1486 bp in length 4926 5925: contig of 2227 bp in length 7753 3929 contig of 2227 bp in length 7753 9190: contig of 2227 bp in length 7753 9190: contig of 2227 bp in length 7754 9190: contig of 1888 bp in length 7755 9190: contig of 1888 bp in length 7751 9190: contig of 1888 bp in length 7751 9190: contig of 1888 bp in length 7751 9190: contig of 1888 bp in length 7752 11018: contig of 1910 bp in length 7753 9190: contig of 1910 bp in length 7754 9190: contig of 1910 bp in length 7755 9190: contig of 1910 bp in length 7757 9190: contig of 1910 bp in length 7758 9190: contig of 1910 bp in length 7759 9190: contig of 1910 bp in length 7750: gpp of unknown length 7750: gpp of unknown length 7750: gpp of unknown length 7750: dength of 1758 bp in length 7750: gpp of unknown length 7750: gpp of u	

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Query Match
Best Local Similarity
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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
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PSA17468
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Best Local Similarity 44.9%; Pred. No. 0.00011;
Matches 396; Conservative 0; Mismatches 481; Indels
                                                                                                                                   /note="assembly_name:Contig37"
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/note="assembly_name:Contig43"

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                                         misc_feature
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
                                                                                                   taggacatactcatgctacacaattatatatcatcactggtcaatcactggtcaatgtgttt 1783
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/organism="Pisum sativum"
/cultivar="Birte"
/db_tref="taxon:3888"
/note="Near-isogenic LOX-2 null line back-crossed"
'Birte'"
                                                                                                                                                                    agcacaattttcaaaaatatcctagtcttcaaccactcaataattcacaatttccaaatc
                                                                                                                                                                                                                                                                                                                                                                      ccttgcaaaacatcacaacctctagaaactttgattaataatctaataaaagcaataata
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                                                                      tctcttcccatgaattcacattgctaaagaaaattaccaccttaaaatgtttatcccttg
                                                                                                                                               1 (bases 1 to 1350)
Forster'C., North,H., Afzal,N., Domoney,C., Hornostaj,A.
Robinson,D.s. and Casey,R.
Wolecular analysis of a null mutant for pea (Pisum sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1350;
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Plant Mol. Biol. 39 (6), 1209-1220 (1999)
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Pred. No. 0.00022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (05-JUN-1998) C. Forster,
Research Park, Norwich, NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Lipoxygenase-2
near-isoline"
238 c 212 q
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Y17468
11poxvonene.
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/gene="lox"
1. .1350
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Matches 130;

ò g DEFINITION

LOCUS

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE

AUTHORS JOURNAL

TITLE

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RESULT AC005083

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Clone CTA-281G5 is from a release of the human BAC library CTB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from VECTOR: pBeloBAC11
                                                        nttp://www.nngri.uiu.gov/Dir/vib/cnr/ , senu
mailto:egreen@hhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                            BAC CTA-281G5 contains an E. coli transposon from 10982 to 12345
    For additional information
                                                                                                                                                                                                                                                                                                                                                        Actual start of this clone is at base position 1 of CTA-281G5; actual end is at 146285 of CTA-281G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     that is not represented in the submitted sequence
                                                     send
                        about the map position of this sequence,
http://www.nhgri.nih.gov/DIR/GTB/CHR7 , s
  University Genome Sequencing Center.
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1891. .7126
                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308. .952
/rpt_family="MER1_type"
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7455. 7481
7456. 7481
7504. 7554
7504. 7554
7504. 7554
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322. .358
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808. .952
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11408. .11526
/rpt_family="(CATAT)n"
11768. .11872
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10759. .11049
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11050. .11235
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264. .1720
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1794. .4826
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466. .8533
rpt_family="AT_rich"
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10581. .10681
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'rpt_family="Alu"
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1946. .10172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="7p15-p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="7"
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                                                                                                                     SOURCE INFORMATION:
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Direct Submission
Submitted (12-JAN-1999) Department of Genetics, Washington
Guiversity, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 146285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 12, 1999 this sequence version replaced gi:3212908.
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                                                                                                                                                                                                                                                                                                                                                                                               AC005083 146285 bp DNA PRI 21-DEC-1999
Homo_sapiens BAC clone CTA-281G5 from 7p15-p21, complete sequence.
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Catarrhini, Hominidae, Homo.
                                           Gaps
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Contact: sapiens@watson.wustl.edu
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Mismatches
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 146285)
Madsen,C. and Blair,T.
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AC005083.1 GI:4150930
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Waterston, R.H.
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REFERENCE AUTHORS

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3203, .23380
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13378..13540
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25826. .25846

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ATPase; NADH dehydrogenase; complete genome; cytochrome b;
cytochrome c oxidase; cytochrome oxidase; mitochondrial genome;
transfer RNA.
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Apis mellifera ligustica complete mitochondrial genome.
L06178
               Indels
            0; Mismatches 491;
 Pred. No. 0.0056;
 44.78;
            Matches 400; Conservative
Best Local Similarity
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LPPSLFMLLLSNLFYDSPGTGWTVYPPLSAYLYHSSPSVDFAIFSLHWSGISSIMGSL NLMYTIMMKNRSMYDQISLFPWSYFITAILIMSLPVLAGAITMLLFDRNRYTSFF DPWGGGDPILYQHLFWFFGHPEVYILILDGFGLISHIVMNESGKKEIFGNLSMIYAML GIGFGFGFIVWAHHMFTVGLDVDTRAYFTSATWITAVPTGKKESLATYHGSKLKINI SILWSLGFINLFTIGGLTGIMLSNSIDIILHDTYYVGHFHYVLSMGAVFAIISFI HWYPLTTGLLNIKWHKIQFIMMFIGYNLFFPOHFIGLMSMPRRYSDYPDSYYCWNS ISSMGSMISLNSMIFLIFILESLISKRMLLFKFNQSSLEWLNFLPPLDHSHLEIPLL IKNLNKSILIKF" Anote="codon recognized: AAU; anticodon unspecified" /product="trNA-OTHER" 3618. 4295 /codon_start=1 /transl_table=5 /product="cytochrome c oxidase subunit 2" /product="cytochrome c oxidase subunit 2" /product="GI:829005" /transl_table=5 /protein_id="AAB96800.1" /db_xref="GI:829005" /translation="MSTWFFFQORSNSYYADNLISFHNWVMMIIMISTLTYVIILD LFMMKFSNLFLLKNHFEIHWHILEIHMINIETHILLILLICFPSLKIYLDEINVNPFSIKSIGH	OWYNSYEY PERNNIEPDSYMINYNNINGFRILETDNRAVIPHKIPLRITTSTDVIHS WTVPSLGIKUDAVPGRINOLNLISKRPGIFFGQCSEICGMNHSFMPIMIESTSFQYFL NWVNQI" 42944362 /note="codon recognized: GAC" /product="trnA-Asp"	/ant.cogon=(pos:432)432/,aa:Asp) 43704438 /ance="codon recognized: AAU; anticodon unspecified" /product="trNA-OTHER" 44414602 /codo_start=1 /transl_table=5 /product="ATPase subunit 8"	id-"AAB96801.1" "GI:829006" ion-"MPQMMPMKWFL art-1 able-5 "ATPaase subunit id-"AAB96802.1" "GI:552442" ion-"MKLILMMNLFR MNFWYNEFKVVSKSKY LWFSFLIXLIYNNYIMNY	LIFESSN. 5285. 6064 /codon_start=1 /transl_table=5 /product="cytochrome oxidase subunit 3" /protein_id="aA896803.1" /db_xref="G1:552443" /translation="MKKNFPFHMVTNSPWPIILSFSFMNTLISTVIMIYSSISMFMIL NFINSILIMMLWFRDIIRESTPGGMHSMFITNFLKFSMILFILSELFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	/note="codon recognized: GGA" /note="codon recognized: GGA" /product="tRNA-G1y" /danicodon="pos:61496151,aa:G1y) 61856538 /codon_start=1 /transl_table=5 /product="NADH dehydrogenase subunit 3" /product="NADH dehydrogenase subunit 3" /protein_id="AAB96804.1" /db_xref="C1:55444" /translation="wkFrFMyFrFTILISSILLLLNKFISTYKKDYFKSSPFECGFN /translation="wkFrFMyFrFTILISSILLLLNKFISTYKKDYFKSSPFECGFN PITKANLPFSLPFFLMTMMFLIFDVEIILFEDIIFYLKSSSTMISYLMISIFLILLIT TLILEWMNNYLNWLF" complement(65726638)
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SOURCE ORGANISM PEFERENCE AUTHORS TITLE JOURNAL MEDLINE FEATURES SOURCE	LRNA LRNA	trnA trnA	trna trna CDS	t RNA	t RNA CDS

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Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
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Catarrhini; Hominidae; Homo.
27-SEP-2000
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On Sep 27, 2000 this sequence version replaced gi:9838025.
Center project name: H_DJ0725G10.
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ns clone RP4-725G10, complete sequence.
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38294 a 29779 c 30262 g 37763.
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AC006970
AC006970.6 GI:10312289
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Waterston, R.H.
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YCSWNLSFYKKNBERMIYILLMAFTKSAQIPFSTWLPMAMAAPTPVSSLVHSSTLVT
AGIYLLIFYVULLDFNYKVITMLIASLTPMLFAGLVANFELDLKKVVAYSTLSQLGFMM
SMLSIGSTELVPLHFFTHAMFKSLMPWCVGSWHYMYSNQDIRMYCOMYYIYPMKSNI
LIFSILSLGGFPFLVGYYSKDLITEMFFSKMIYFSMINLIGTIFTVSYSFRMILVL
TSKFLMMNVITSKEDRIMOLISMMMMTFSLITSKLFPLMMFNYLLGINFTKLMY
KMINGLLIMGFNFYLILLNNKIGYFKMSFLFNLMNFNYKIIMMFTYEVYIEKS
TIEILGSKFMSYTLILLNNKIGYFKMSFLFNLINYKIIMMFTYEVYIEKS
TIEILGSKFMSYTLILLNYTGLFKMSFLFNLIYKIITMMFTYEVYIEKS
COMPLEMENT (8557. 8624)
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YYGSMILASIMLKLGGYGMLRLMIIYKNEFILIQKILVMINSFGVLILSLMCLSQFDM
KSIIAISSIVHMGLMIMSMMTFLKISLIGGYLMMISHGLSSSGLFFLVNVIYSQTNSR
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YCLFSFIYSIYLFMFINHGKIFIMFKIKNGILVEYFVLLLHWIPLNLMFLKLYFI"
complement(9991. .10254)
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                                                                                                                                                                                                                                                                                                           /translation="MIKMMVCGILFFEFSFLMMLMSLYLLYLNKFFFFEWNIYTFNSM
KFNFLLLIDYKSLMFIFVSMIIYSISYMDLSELKMDRFLYLMILFLISMYML
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ISLLLVFLSMNLLLFYLFYEFGLLLIFYLVVKWGYSENRWLSGFYLMFYTMIFSLPML
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                                                                                        /product="tRNA-Asi"
/anticodon=(pos:6765, .6767,aa:Asn)
complement(6810, .6878)
/note="codon recognized: AUU; anticodon unspecified"
/product="tRNA-OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="NADH dehydrogenase subunit 4"
/protein_id="AAB96806.1"
/db_xref="G1:552446"
                                                                                                                                                                                                                                 /transl_table=5
/product="Nabl dehydrogenase subunit 5"
/protein.id="AAB96685.1"
/db_xref="GI:829007"
                                        .6604, aa: Arg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /anticodon=(pos:8589. .8591,aa:His)
complement(8644. .9987)
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/product="tRNA-His"
                                                          6734. .6802
/note="codon recognized: AAC"
    /note="codon recognized: AAG"
                                                                                                                                                                                           complement(6892. .8556)
                                        /anticodon=(pos:6602.
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/transl_table=5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113611 ААААТАСАТАТААТАТАТАТАЛАААТАТАТАТАТАТАТАСАТААААТААТААТААТАТААДААТ 113670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 113850 TATAAAATATATATATATATATATATGATATGTATTTTATATATATATATGTATTTTA 113909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1909 tattittgcattitcaaaaactaaaccaaaccaaacttagaatattitgtaattatagcac 1968
                                                            1253 ataccattaatagatcactttgaatggatatcattcatactatatcaaacatttacgtaa 1312
                                                                                                                                                                                                                                                                                                                        tttaatatatatetegteatgtgtgggtggatteaatttaattgtategtaaatggtagga 1728
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                                                                                                               1313 agataaaaaattcacccaaacaaatgagagagacactacatctcttattata----tt
                                                                                                                                                                   aataaaatgtaaagaaaaatatagtataaaagtaacacatattttgataaatttattact
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                                    . 9
                                   0; Mismatches 596;
          6
         Score 71.4; DB 9 Pred. No. 0.0082;
         Query Match 3.1%;
Best Local Similarity 43.6%;
Matches 465; Conservative
         Query Match
Best Local Similarity
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Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W.

By Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W.

Direct Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology

Center, Stanford University, 855 California Avenue, Palo Alto, CA -
94304, USA

On Aug 12, 2000 this sequence version replaced gi:8810451.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* This record will be updated with the finished sequence.
                                                                                                                                                                                              Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                      malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 245802)
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Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T., Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
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7569 147768: gap of unknown length

7769 217470: contig of 69702 bp in length

4471 217670: gap of unknown length

7671 219372: contig of 1702 bp in length

9573 219372: contig of 1702 bp in length

9573 221333: contig of 1761 bp in length

134 221533: gap of unknown length

134 445802: contig of 1761 bp in length

Location/Qualifiers
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0; Mismatches 469;
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/organism="Plasmodium
/db_xref="taxon:5833"
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HTG; HTGS_PHASE1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160788)
Mclay, K.
111883 TAATTTTATCTATATATATATATACAATCTATTTATATATAAAATATATATATATTT 111942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 112003 ATTTATTTACCATATTTTTATTATATTATAAAAACAGCATCACATTAATGCAGAAAC 112062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 112121 ATATAATATATATAAAATTTTTTTTTTAACAAATAAAATATAAATATTACATGTAATATTTT 112180
                                                                                                 Db 112181 ACAAAAATATAAAAAATAACAAGAAATATTTAATTATGTAAAAATTAACAAAAAATAAT 112240
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                                                                                                                                                                                                                                        tgttcttttataacgtttgtctatgccgtattacccatatggtcactagaatgggacaat 1665
                                                                                                                                                                                                                                                                                                                                                                                                                ggacatactcatgctacaca-attatatcatcactggtcaatcactggtcaatgtgtttt 1784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2001
*** SEQUENCING IN
                                                                                                                                                                              1905 caattatttttgcattttcaaaactaaaccaaacaaacttagaatattttgtaattata
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Homo sapiens chromosome 1 clone RP11-269F19,
PROGRESS ***, 9 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_FULLTOP
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JOURNAL
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator E-amersham; 2% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Consensus quality: 158006 bases at least Q40
Consensus quality: 158812 bases at least Q30
Consensus quality: 159376 bases at least Q20
Insert size: 159988; sum-of-contigs contigs Contigs Quality coverage: 9.97x in Q20 bases; sum-of-contigs Quality
Coverage: 9.32x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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43404 64554: contig of 21101 bp in length

64505 64601: gap of 100 bp

64605 95591: contig of 31087 bp in length

95692 95791: gap of 100 bp

95792 118401: contig of 22610 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 4065: contig of 4065 bp in length
4066 4165: gap of 100 bp
4166 17933: contig of 13768 bp in length
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18034 43303: contig of 25270 bp in length
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136017: contig of 17516 bp in length
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fragment_chain:1"
18034. ...43303
/note="assembly_fragment:00012
fragment_chain:1"
// note="assembly_fragment:00094
fragment_chain:1"
// note="assembly_fragment:01356
fragment_chain:1"
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//note="assembly_fragment:01760
fragment_chain:3"
136118. .145258
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fragment_chain:1"
4166. .17933
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/note="assembly_fragment:01103
fragment_chain:2"
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fragment_chain:3"
145359, .160788
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fragment_chain:3
Center project name: bA269F19
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/db_xref="taxon:9606"
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118502 1360
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     Direct Submission
Submitted (28-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 153705 bases at least Q40
Consensus quality: 153756 bases at least Q30
Consensus quality: 154302 bases at least Q20
Insert size: 155533; sum-of-contigs
Insert size: 155533; law error; agarose-fp
Quality coverage: 6.73x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                               On Jul 30, 2001 this sequence version replaced gi:15028764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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133977 156133: contig of 22157 bp in length.
                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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fragment_chain:1"
3298. .24805
/note="assembly_fragment:00590
fragment_chain:1"
24906. .27453
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fragment_chain:1"
27554. 64419
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/note="assembly_fragment:03269
fragment_chain:1"
64520. .84883
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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1. .3197
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/db_xref="taxon:9606"
/chromosome="1"
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  AL593856.6 GI:15041959
                                                                                                   Mammalia, Eutheria, Pr. 1 (bases 1 to 156133) Mclay, K.
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                                                                                                                                                                          9;
                                                                                                                              Length 160788;
                                              others
                                                                                                                     2.9%; Score vv,
43.5%; Pred. No. 0.03;
+ive 0; Mismatches 465; Indels
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                  vector_side:right"
| 38964 c 40180 g 40496 t
clone_end:T7
                                                                                                                                                                          Matches 363; Conservative
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                                           40346 a
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DEFINITION
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JOURNAL
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                          1318 aaaaattcacccaaacaaatgagagagacactacatctctcttattattaataataga 1377
                                                                                                                                                                                                                                                                                                         1378 taaagaaaaatatagtataaaaagtaacacatattttgataaatttattactaaaactatt 1437
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                                                                                                              600 others
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                                                                                                                                                                       Pred. No. 0.032;
0; Mismatches 542;
/note="assembly_fragment:03551
fragment_chain:1"
#984. .133876
/note="assembly_fragment:01981
fragment_chain:1"
133977. .156133
                                                                                                                                                             DB 2;
                                                                                                vector_side:right"
| 32182 c 32348 g 44855 t
                                                                                                                                                          Query Match 2.9%; Score 67.8;
Best Local Similarity 41.6%; Pred. No. 0.0
Matches 395; Conservative 0; Mismatches
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Buouffard, G.G., Dietrich, N.L., Eagle, W.O., Gupta, J., Ho, S.-L.,
Huang, M.C., Idol, J., Lee-Lin, S.-O., Maduro, O.L., Maduro, V.B.,
Mastrian, S.D., McCloskey, J.C., Morse, E., Ojodu, M.A., Pearson, R.,
Stantripop, S., Summers, T.J., Thomas, J.W., Thomas, P.J.,
Tiongson, E.E., Tucchman, J.W., Tran, J.T., Vogt, J.L., Walker, M.A.,
Wetherby, K.D. and Green, E.D.
NISC Mouse Sequencing Initiative
2087 tatctaaacaatatcaccatatatgttatgatataatatgatgcagcaatacacttaatt 2146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Center, 8717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 195465 bases at least Q40
Consensus quality: 197294 bases at least Q30
Consensus quality: 198466 bases at least Q30
Consensus quality: 198466 bases at least Q30
Insert size: 200900; agarose-fp
Insert size: 206384; sum-of-contigs
Quality coverage: 6.43x in Q20 bases; agarose-fp
Quality coverage: 6.51x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                     07-JUN-2000
                                                                                                                                                                                                                                                                            HTG 07-JUN-200
6 clone RP23-189E15 strain C57BL6/J,
24 unordered pieces.
                                                       27002 ATATATADAATTATACAAAATTTATATATATAAAATATAAAATATACATAAAAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                         26942 ATATATATATATATAAATAATATATATATATATATAAATACATA 26894
                                                                                                             2147 tggtaaagcattaaagcgagacaactctattaacaccggtaattcaaca 2195
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Center clone name: 189E15
                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT.
house mouse.
                                                                                                                                                                                                                                                                                                                         Mus musculus chromosome WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                 AC072048
AC072048.1 GI:8313202
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AC072048/c
LOCUS
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RESULT 13
                                                                                                                                                                                                                               of 11607 bp in length funknown length of 9282 bp in length funknown length funknown length of 14166 bp in length
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f unknown length
g of 12071 bp in length
f unknown length
of 14807 bp in length
f unknown length
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bo in length
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g of 8485 bp in length
f unknown length
g of 9020 bp in length
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gap of unknown length
contig of 14675 bp in length.
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bp in length
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unknown length
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bp in length
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1. .2209
/note="assembly_fragment"
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of 9319
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note="assembly_fragment"
606. .14706
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .208684
/organism="Mus musculus"
/strain="C57BL6/J"
/db_xref="taxon:10090"
/chromosome="6"
/clone="RP23-189E15"
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note="assembly_fragment"
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/note="assembly_fragment"
64543. .73027
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|5124. 64442
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1727 gacatactcatgctacacaattatatcatcactggtcaatcactggtcaatgtgttttct 1786
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                                                                                                                                                                                                                                                                                                                                                                                                                2323 others
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48824 c 48605 g 54542 t
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140809...151652
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151753...163823
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163924...178730
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32248. .93854
                                                                                                                   117603. 130162
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130263. 140708
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178831. .193909
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194010. .208684
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                                                                                                                                                                                                                                                                                                                                    Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USB.

**NOTE: This is a "working draft" sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as *runs of N, but the exact sizes of the apps are unknown.

* This record will be updated with the finished sequence * This record will be updated with the finished sequence is soon as it is available and the accession number will
                 AC005506 205429 bp DNA HTG 12-AUG-2000
Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
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malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota: Alveolata: Apicomplexa: Haemosporida; Plasmodium.
1 (bases 1 to 205429)
                                                                                                                                                                                                       Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T.,
Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
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Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
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    .205429
    /organism="Plasmodium falciparum"
/db_xref="taxon:5833"

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Submitted (24-FBB) 1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge (B10 18A, UK)
On Aug 12, 1999 this sequence version replaced gi:5531400.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M.
and Barrell,B.
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*** SEQUENCING
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                                                                                                                                                                                                                                                                                                                       84101 ААААААССААААААААААААААААААААААААТСАТААААТСАБААСТЯТАААААТААТ
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Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFMAL4P4 224448 bp DNA HTG Plasmodium falciparum chromosome 4 strain 3D7, PROGRESS ***, in unordered pieces.
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    .224448
    /organism="Plasmodium falciparum"

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HTG; HTGS_PHASEL.
malaria parasite P. falciparum.
Plasmodium falciparum
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                                             Score 66.6; DB 2; Length 2
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/chromosome="4"
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Best Local Similarity 20.1
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Consensus quality: 31111 bases at least Q40
Consensus quality: 31874 bases at least Q30
Consensus quality: 31871 bases at least Q20
Consensus quality: 31871 bases at least Q20
Estimated insert size: 42980; agarose-fp estimation
Estimated insert size: 34477; sum-of-contigs estimation
Quality coverage: 5.56 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
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Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute.

Direct Submission

Direct (03-JUL-2001) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Center Project Name: 31883, FOS36853
Center clone name: LLNL-FOS_20C5
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Mammalia; Eutheria; Primates; Cata
1 (bases 1 to 36977)
Deb Joint Genome Institute.
Sequencing of Human Chromosome 19
Unpublished
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Center: Joint Genome Institute
Center Code: JGI
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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GenCore version 4.5
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SUMMARIES

Description	Sequenc	1CKen C-m TAF-3873-	HGC	HOMO S	ouatta p MSS31 Mo	U38679 Avian infec	vian	vian in	AU023328 Rattus no D28849 Hepatitis C	infect	HGC-1013	uman chr HGC-8077	dneuc	nome DNA	AC061540 Giardia i AX187114 Seguence	Nyctea s	AF231331 AS10 Otus AC038063 Giardia i	Drosophi	Arsos4ss Fusarium AF363432 Fusarium	AF069970 Nasalis 1	Glardi Phytol	Homo s	ACU81006 Glardia 1 AC032864 Giardia i	Giardi	Giardi	Giardi Seguen	AX099541 Sequence	Sequ	מו מו		PAT 24-AUG-2000	i I					RIE PASCALE (FR)	." amplification of NGA249 SSLP	
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Presoak: 94 degrees C for 4.00 minutes
Denaturation: 94 degrees C for 50.0 seconds
Annealing: 58 degrees C for 1.50 minutes
Polymerization: 72 degrees C for 1.00 minutes
PCR Cycles: 30
Thermal Cycler: custom built by IAS, Costar, Cambridge MA
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/db_xref="taxon:9606"
/map="68,70 cm from top of Chr19 linkage group"
/clone_lib="Human THudson SANGER"
/note="human STS created from EST in the Sanger database"
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164)
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SHGC-130652 Human Homo sapiens STS genomic, sequence tagged site.
G59874
Stein, L., Hsie, L., Topaloglou, T., Hubbell, E., Robinson, E., Mittmann, M., Morris, M.S., Shen, N., Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M. and Lander, E.S.
                                                                                        Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome Science 280 (5366), 1077-1082 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 164;
                                                                                                                                                                 Synonyms: stSG28550
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
                                                                                                                                                                                                                                        9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
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                                                                                                                                                                                                                                                                                              Email: thudson@genome.wi.mit.edu
Primer A: TTTGATAAGCTGGTGAGGTGC
Primer B: TGGTGCCTTATCCCAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Template: 10 ng
Primer: each 5 pM
dNTPs: 4 nM
Taq Polymerase: 0.5 U
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G59874/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 164)

Wang, D. G., Fan, J. B., Siao, C. J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Perkins, N., Winchester, E., Spencer, J., Kruglyak, L.,
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G44227 164 bp DNA STS 28-JAN-1999 WIAF-3873-STS Human THudson SANGER Homo sapiens STS genomic, sequence tagged site.
G44227 G44227 G1:4193144
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Nucleotide sequence analysis of the chicken gene c-mil, the progenitor of the retroviral oncogene v-mil

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O
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8 of 11
Chicken DNA, clones lambda c-mil-4 and lambda c-mil-7.

    139
    note="c-mil protein, (putative); putative"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 12; DB 5; Length 145; ilarity 100.0%; Pred. No. 5.2e+03; Conservative 0; Mismatches 0; Indels
               marker in Arabidopsis thaliana subspecies" ^{\prime} C ^{\prime} 3 g ^{\prime} t
                                                                                                         100.0%; Score 12; DB 6; Length 22; 100.0%; Pred. No. 5.9e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   VRT
                                                                                                                                                                                                                                                                                                               CHKMILO8 145 bp DNA
Chicken c-mil proto-oncogene, exon 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="c-mil intron H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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K03266.1 GI:212316
                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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21 GGATTTTACAGT 10
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nes 12; Conserv
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Centro de Biologia Molecular, Cantoblanco, Madrid 28049, SPAIN 2 (bases 1 to 215)
Rodriguez-Pombo,P., Hoenicka,J., Muro,S., Perez,B., Perez-Cerda,C., Richard,E., Desviat,L.R. and Ugarte,M.
Human PCCB gene:exon-intron definition and mutational spectrum in Spanish and Latin American propionic acidemia patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 220)
Ellsworth,J.A., Pratt,S.A., Constable,J.L. and Hoelzer,G.A.
Simple sequence repeat (SSR) PCR primers found in mantled howling
monkeys (Alouatta palliata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alouatta palliata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 220)
Hoelzer,G.A.
Direct Submission
Submitted (26-ARR-1994) Guy A. Hoelzer, Biology, University of
Nevada Reno, Reno, NV 89557, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Alouatta palliata clone Ap6 simple sequence repeat region.
U09224
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ilarity 100.0%; Pred. No. 5.1e+03;
Conservative 0; Mismatches 0;
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Pred. No. 5.1e+03;
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/db_xref="taxon:30589"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                 1. .215
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                      /usedin=AJ006487:cdspccb
                                                                                                                                                                                                                                                                                                       /usedin=AJ006487:rnapccb
                                                                                                                                                                            /cell_type="fibroblast"
65. .121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="blood"
/dev_stage="adult"
28 c 32 q
                                                                                                                   Location/Qualifiers
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ilarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mantled howler monkey.
                                                                                                                                                                                                           /gene="PCCB"
65. .121
                                                                                                                                                                                                                                           /gene="PCCB"
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Ugarte, M.
Direct Submission
Submitted (22-MAY-1998) Ugarte M., Universidad Autonoma de Madrid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                                            minutes
                                                               Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgo.stanford.edu
Primer A: GAGGTGCTTTGCTTGTTCCTTA
Primer B: GTCCTTATCCCAACATTTCTGA
STS size: 148
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 164;
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                                                                                                                                                                                                                                      95 degrees C for 10 m
94 degrees C for 30 s
60 degrees C for 30 s
72 degrees C for 23 s
30
Perkin Elmer 9700
                                                                                                                                                                                                                                                                                                                                               25 ng
each 1 uM
each 200 uM
0.07 units/ul
5 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRI
                    Unpublished, Olivier, M., Cox, D.R. (2000)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 12; DB 11;
100.0%; Pred. No. 5.2e+03;
ive 0; Mismatches 0;
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Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19"
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50 mM
10 mM
8.3
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15. .162
15. .37
                                                                                                                                                                                                                                         Initial incubation:
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Annealing:
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (140.
                                                                                                                                                                                                                                                                                                    PCR Cycles:
Thermal Cycler:
         Olivier, M. and Cox, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCl:
Tris-HCl:
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Best Local Similarity 100.
Matches 12; Conservative
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

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RESULT G48131/c LOCUS

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ACCESSION VERSION

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/product="spike protein"
/protein_id="AaB47437.1"
/db_xref="G1:1055306"
/translation="GWHLHGGAYAVVIFFRTNNAGAASECTNGIISGGSGFNASSIAM
TAYOPGMQWSKSQFTAHCNFSPTVFTH"
1 40 54 9 80 t
                                                                                                                                                                    Avian infectious bronchitis virus.
Avian infectious bronchitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-OCT-1995) Ching-Ho Wang, National Taiwan University, Vetrinary Medicine, 142 Chou-san Rd., Taipei, 106, Taiwan Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian infectious bronchitis virus.

Avian infectious bronchitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                           Wang, C.H. and Tsai, C.T.
Genetic grouping for the isolates of avian infectious bronchitis
virus in Taiwan
Arch. Virol. 141 (9), 1677-1688 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (sites) Wang, C.H. Wang, C.H. and Tsai, C.T. Genetic grouping for the isolates of avian infectious bronchitis
                             AIU38679 228 bp RNA VRL 14-FEB-1997
Avian infectious bronchitis virus All71 spike protein (S1) gene,
hypervariable region 1, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIU38677 231 bp RNA VRL 14-FEB-1997 Avian infectious bronchitis virus Al211 spike protein (S1) gene, hypervariable region 1, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .228
/organism="Avian infectious bronchitis virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="S1"
/note="hypervariable region 1; N-terminus"
/codon_start=2
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100.0%; Pred. No. 5.1e+03;
ive 0; Mismatches 0;
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Arch. Virol. 141 (9), 1677-1688 (1996)
97049060
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/db_xref="taxon:11120"
1. .228
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Wang, C.
                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 228)
Wang, C.
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0
                                                                                          G48131 222 bp DNA STS 09-APR-1999 SMSS31 Mouse EGreen Mus musculus STS genomic, sequence tagged site.
                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (2022)
DeSilva,U., Massa,H., Trask,B.J. and Green,E.D.
Comparative Mapping of the Region of Human Chromosome 7 Deleted in William's Syndrome
Unpublished (1999)
Synonyms: 92N10R
Contact: Eric D. Green
                                                                                                                                                                                                                                                                                                                                                                             Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing
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Denaturation: 92 degrees C for 0.17 minute(s)
Annealing: 58 degrees C for 1.00 minute(s)
Polymerization: 72 degrees C for 1.00 minute(s)
PCR Cycles: 35
Thermal Cycler: PerkinElmer 9600
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100.0%; Score 12; DB 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 12; Conservative 0; Mismatches 0;
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each 1 uM
each 200 uM
0.05 units/ul
10 ul
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/clone_lib="Mouse EGreen"
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: egreen@nhgri.nih.gov
Primer A: TGCCTCTAGTCAGGATTGCC
Primer B: AGATGCTTGGTTGGGTAGGTG
STS size: 222
PCR Profile:
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100 mM
10 mM
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81 GGATTTTACAGT 70
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/product="spike protein"
/protein_id="aAB47439.1"
/protein_id="aAB47439.1"
/db_xref="C1:1055310"
/translation="GWHLHGGAYAVVNVSSQTNNAGTAQGCTVGIISGDRVVNASSIA
MSAPVGQMQWSKSQFCTAHCNFSDFTVFVTH"
MSAPVGQMQWSKSQFCTAHCNFSDFTVFVTH"
                                                                                                                                                                                                                                                                                                                    Avian infectious bronchitis virus.
Avian infectious bronchitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-67-1995) Ching-Ho Wang, National Taiwan University,
Vetrinary Medicine, 142 Chou-san Rd., Taipei, 106, Taiwan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         1 (sites) \mbox{\it Wang,C.H.} and \mbox{\it Tsai,C.T.} Genetic grouping for the isolates of avian infectious bronchitis
                                                                                                                                                                                                                     AIU38681 231 bp RNA VRL 14-FEB-1997 Avian infectious bronchitis virus A1955 spike protein (S1) gene, hypervariable region 1, partial cds.
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Rattus norvegicus, OTSUKA clone, OT57.23/887g03, microsatellite
sequence, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Avian infectious bronchitis virus"
/strain="A1955"
/db_xref="taxon:11120"
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/gene="S1"
/note="hypervariable region 1; N-terminus"
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Rattus norvegicus
                                     100.0%; Score 12; DB 14;
llarity 100.0%; Pred. No. 5.1e+03;
Conservative 0; Mismatches 0;
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97049060
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U38681.1 GI:1055309
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                                                                                                                                                                                                  /product="spike protein"
/protein_id="AaB47436.1"
/db_xref="GI:1055304"
/translation="GWHLHGGAYAVVNVSSETNNAGSASACTVGIISGGRIVNASSIA
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Direct Submission
Submitted (17-0cT-1995) Ching-Ho Wang, National Taiwan University,
Vetrinary Medicine, 142 Chou-san Rd., Taipei, 106, Taiwan
Location/Qualifiers
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Submitted (17-OCT-1995) Ching-Ho Wang, National Taiwan University,
Vetrinary Medicine, 142 Chou-san Rd., Taipei, 106, Taiwan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIU38678 231 bp RNA VRL 14-FEB-1997
Avian infectious bronchitis virus A1960 spike protein (S1) gene,
hypervariable region 1, partial cds.
U38678
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Wang,C.H. and Tsai,C.T.
Genetic grouping for the isolates of avian infectious bronchitis
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/strain="A1960"
    /db_xref="taxon:11120"

                                                                             /organism="Avian infectious bronchitis virus"/strain="A1211"
/db_xref="taxon:11120"
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/note="hypervariable region 1; N-terminus"
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Pred. No. 5.1e+03;
Mismatches 0;
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Avian infectious bronchitis virus
Viruses; ssRNA positive strand viruses,
Coronaviridae; Coronavirus.
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Best Local Similarity 100.
Matches 12; Conservative
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205 GGATTTTACAGT 216
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/gene="S"
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Matches 12; Conservative
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                                                                                                                                                                                                                 Submitted (24-JUL-1998) to the DDBJ/EMBL/GenBank databases. Takeshi K Watanabe, Otsuka Pharmaceutical Co., Ltd., Otsuka GEN Research Institute; 463-10, Kaqasuno, Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan (E-mail:watanebectsuka.genome.ad.jp, Tel:81-886-65-2888, Fax:81-886-37-1035)
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Hepacivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-MAR-1994) to the DDBJ/EWBL/GenBank databases. Kazuo Agifyuma. National Cancer Center Research Institute, Virology Division; 5-1-1, Tsukiji, Chuo-ku, Tokyo 104, Japan (Tel:03-3542-2511(ex.4701), Fax:03-3543-2181)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama, K., Kato, N., Nakazawa, T., Yonemura, Y., Phornphutkul, K., Kunakorn, M., Petchclai, B. and Shimotohno, K.
Novel genotypes of hepatitis C virus in Thailand
J. Gen. Virol. 76 (Ft 9), 2323-2327 (1995)
                                               1 (sites)
Watanabe,T.K., Hishiqaki,H., Kanemoto,N., Miyakita-Mizoguchi,A.,
Oga,K., Okuno,S., Ono,T., Tsuji,A., Hayashi,H., Adachi,M.,
Yamasaki,Y., Iriye,Y., Takahashi,E., Takagi,T., Nakamura,Y. and
                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
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/note="0T57.23/887903F=5'-CCTTATTTCCATGGTACCTGA-3',
0T57.23/887903R=5'-CGATCAGGTACTTGCCATACC-3'"
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                                                                                                                                The large-scale mapping of rat microsatellite markers
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Hepatitis C virus RNA for NS5, partial sequence.
D28849.1 GI:1009306
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/organism="Hepatitis C virus"
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Hepatitis C virus (strain:TH13) RNA.
Hepatitis C virus
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/db_xref="taxon:11103"
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1. .285
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    .366
    /gene="TH13PI"
    .>366

                                                                                                                                                Unpublished (1998)
2 (bases 1 to 285)
Watanabe, T.K.
Direct Submission
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Matches 12; Conservative
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RAVRAKLIAQGGKAAICGRY"
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CNFTDFTVFVTHCFKSGAGQCPLTGFLPSGVIRVSAMRKGNTSLFYNLTVSVTKYPTF
                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviradae; Coronavirus.

Coronaviradae; Coronavirus.

1 (bases 1 to 368)

Capua, L., Minta, Z., Karpinska, E., Mawditt, K., Britton, P.,

Cavanagh, D. and Gough, R. E.

Co-circulation of four types of infectious bronchitis virus (793/B, 624/I, B1648 and Massachusetts)

Avian Pathol. 28, 587-592 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBR243261 368 bp RNA VRL 31-JAN-2000 Infectious bronchitis virus S gene, strain 624/I (368bp). AJ243261
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Capua, I.
Direct Submission
Submitted (18-JUN-1999) Capua I., Instituto Zooprofilat
Venezie, Via Romea 14/A, 35020, Legnaro, Padova, Italy
Location/Qualifiers

    .368
    /organism="Avian infectious bronchitis virus"

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                                                                                                                                                                                                                                                                                        Length 366;
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iive 0; Mismatches 0;
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/db_xref="taxon:11120"
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-- Washington University/Merck EST sequence.
Location/Qualifiers
1. 388
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="13"
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 388) Myers, R.M. Unpublished (1996)
                05-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                          Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                          Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259689
Fax: 415726689
Email: myers@shgc.stanford.edu
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           G30656 388 bp DNA STS human STS SHGC-37261, sequence tagged site. G30656. G1:1594207 STS; STS sequence; primer; sequence tagged site. human.
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each 1 uM
each 200 uM
: 0.05 units/ul
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Primer B: CTTTGCAGTTATTGCTAGATGGG
STS size: 128
PCR Profile:
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50 mM
20 mM
8.3
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10. .33
complement(115. .137)
a 74 c 68 g
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Polymerization:
PCR Cycles:
Thermal Cycler:
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Total Vol:
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GenCore version 4.5 Copyright (c) 1993 · 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

April 3, 2002, 04:39:12 ; Search time 2120.21 Seconds (without alignments) 471.348 Million cell updates/sec

US-09-700-187-2

1 aaaagtaacacatattttga.....ttacagtaataagaaacga Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

11351937 seqs, 5372889281 residues Searched:

22703874 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

em_gss_hum:*
em_gss_inv:*
em_gss_pln:*
em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
em_gss_vrt:* 1: em_estfun:*
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11: gb_est2:*
12: gb_htc:*
13: gb_gss:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		AA169463 zo84h08.r	BH036705 RPCI-24-2	BH102413 RPCI-24-2	AL239097 Tetraodon	BG024018 602303237	C90222 C90222 Dict	AV405634 AV405634	AQ776172 HS_5571_A	AQ743241 HS 5388 B	AQ764101 HS 2001 A	AJ388941 AJ388941	A0545066 CITBI-E1-
			.69463	36705	.02413	103DHC	124018	1222	.05634	AQ776172	43241	64101	188941	45066
	1		0 AA1	3 BH0	3 BH1	3 CNS	1 BG0	1 C90	0 AV4	3 AQ7	3 AQ7	3 AQ7	0 AJ3	3 AO5
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	Query Match Length DB ID		357	320	555	489	1714	521	631	442	846	515	587	545
æ	Query		40.6	39.1	39.1	38.1	38.1	37.4	37.2	37.0	36.6	36.1	35.9	35.7
	Score		37.8	36.4	36.4	35.4	35.4	34.8	34.6	34.4	34	33.6	33.4	33.2
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AV739051 AZ648187 TA195A02P TA12F02P BG025969	CNSO5FLS B56628 B12729 B10407	BE030084 AZ334849 AZ516773 CNS00LU6	CNS0050Y BG555297 BE873019 AV017830 BE217602 CNS0605W	ALS.4586 CNSO1667 A1699725 F02028 N73114 A103873 R92539 AW512010 A1200734	AW010162 H47009 R52980 N55097
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ALIGNMENTS

AA169463 357 bp mRNA EST 09-NOV-1997 2084h08.rl Stratagene ovarian cancer (#937219) Homo sapiens CDNA clone TMAGE.593631 5', mRNA sequence.	AA169463.1 GI:1748411 EST. human.	Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia: Eutheria: Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 357) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,	Taximan, D., Kucaba,T., Lacy, M., Leo, N., Lennon,G., Marra,M., Martin, J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Whashu-Nci human EST Project Uppublished (1997) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800	Fax: 34 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1082
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RESULT 1 AA169463/C LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT	FEATURES SOURCE

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Gaps

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31;

Length 320; Indels

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BH102413 555 bp DNA GSS 19-JUL-2001
RPCI-24-229N23.TJ RPCI-24 Mus musculus genomic clone RPCI-24-229N23
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Wector by Library produced by Pieter de Jong. The
RIDrary was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhoo@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 229 row. N column: 23
Seq primer: SP6
Class: BAC ends.
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other, GSSs: RPCI-24-229N23.TV
Contact: Shaying Zhao
Department of Eukaryctic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 555)
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ilarity 64.0%;
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Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 4000 Fax: 4000 Fax: 4000 Fax: 4000 Fax: 4000 Fax: 4
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RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBACI cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
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RPCI-24-22406.TJ RPCI-24 Mus musculus genomic clone RPCI-24-22406,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 aaaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc 60
/clone_lib="Stratagene ovarian cancer (#937219)"
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ilarity 64.0%; Pred. No. 37;
Conservative 0; Mismatches 32;
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BH036705.1 GI:14811846
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Dictyostelium discoideum
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                                                        mRNA sequence.
BG024018
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fi/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                           GSS; genome survey sequence.

Tetraodon nigroviridis.

Tetraodon nigroviridis

Tetraodon nigroviridis

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

[ (bases 1 to 489)

Rosest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Weissenbach,J.
                                                                                                                                                                                                                              CNSO3DHC 489 bp DNA GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
017A03 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Terraodon nigroviridis DNA sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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                                        Gaps
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                  1 aaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Tetraodon nigroviridis"
//db.xref="taxon:99883"
/clone="017A03"
/clone_lib="G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.4; DB 13;
Pred. No. 1.1e+02;
; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
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                                                                                                                               216 TTCCTTAAGTTATTAGCAGCAATAGA 241
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                                                                                             atgictgaggattttacagtaataaa 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.1%;
64.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 tgaggattttacagtaata 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genòscope
                                                                                                                                                                                                                                                                                                             AL239097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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BASE COUNT

ORIGIN

Matches

g ŏ

δ

37

RESULT

AUTHORS TITLE JOURNAL

FEATURES

JOURNAL REFERENCE

TITLE

SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS

TITLE

LOCUS

ACCESSION VERSION KEYWORDS

CNS03DHC/c

RESULT

61

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QQ

g

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Eukaryota; Mycetczoa; Dictyostellida; Dictyostellium.

1 (bases 1 to 521)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Loppublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov
Plate: LLAM10090 row: j column: 09

High quality sequence stop: 30.

Location/Qualifiers

rce
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1714)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="InActions"
/clone="InActions"
/clone=lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/tissue_type="duodenal adenocarcinoma, cell line"
/tab_host="DH108 (phage-resistant)"
/note="Organ : small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: Sal; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
a 209 c 457 g 129 t
BG024018 1714 bp mRNA EST 24-JAN-2001 602303237F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4394600 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C90222 521 bp mRNA EST 20-APR-1998 C90222 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SS1395, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.1%; Score 35.4; DB 11;
61.3%; Pred. No. 80;
1ive 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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JOURNAL
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Indels

1.6e+02; thes 34;

29-JUL-1999 BAC Library Homo sapiens DNA sequence.

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1 (bases I to 442)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (206) 616-3618
Fax: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genelics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and
                                                                                    1 aaaagtaacacatattttgataaatttattactaaaactatttctagtacttgttaatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington Assanides Assanides Assanides North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                   AQ776172 442 bp DNA
HS_5571_A2_G04_T7A RPCI-11 Human Male
genomic clone Plate=1147 Col=8 Row=M,
    Pred. No. 1.66
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 442.
Location/Qualifiers
                                                                                                                                                                                 149 AAGAATGAAACATAAATAATTAAAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 1147 row: M column: 8
                                                                                                                                            61 atgtctgaggattttacagtaataaagaa
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                        0
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63.1%;
      61.8%;
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                        Conservative
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
    Local Similarity
nes 55; Conserv
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LOCUS
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      Best Loc
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COMMENT
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KEYWORDS
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                                                                                                   a
                                                                                                                                            Qγ
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1 (bases 1 to 631)

Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method:uni-directional, sequence direction:sequenced from T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV405634 631 bp mRNA EST 06-FEB-2000 AV405634 Bombyx mori cohna clone wdv30047 T3, mRNA sequence.
AV405634 GI:6909722
                                                                                                                                                                                                  /clone="SS1395"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Bombyx mori wing disk C108 5th-instar day-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5' -> 3')
Project='Silkworm Genome Program in MAFF, and Research for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           13 tattttgataaatttattactaaaactattttctagtacttgttaatcatgtctgaggat 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Future Program in JSPS'. see 'Silkbase',
chttp://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.
                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                          Score 34.8; DB 11; Length 521;
Pred. No. 1.5e+02;
0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                1 others
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Taskuba
University of Taskuba, Ibaraki 305, Japan
Email: 4402hu@sakura.cc.tsukuba.ac.jp.
                                                                                                                                    /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="wing disk"
/dev_stage="5th-instar day-3 larva"
94 c 68 g 231 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                ų
                                                                                                                                                                                                                                                                135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="female/male mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bombyx mori"
                                                                                                                                                             /strain="AX4"
/db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C108"
/db_xref="taxon:7091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="wdV30047"
                                                                                                                                                                                                                                                                                                                                            37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || | | | ||||||| ||| 479 TAATAATAAAAA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 tttacagtaataaagaaa 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domestic silkworm.
                                                                                                                                                                                                                                                                                                                                            Query Match 37.4
Best Local Similarity 65.4
Matches 51; Conservative
                                                                                                                                                                                                                                                                253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
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                                                                                                                            source
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ORGANISM
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DEFINITION
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ORIGIN
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VERSION
KEYWORDS
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TITLE
JOURNAL
COMMENT
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ORIGIN
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                                                                                                     FEATURES
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    COMMENT
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/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 5 others
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                          8 acacatattttgataaatttattactaaaactattttctagtacttgttaatcatgtctg 67
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                          442;
                               /clone="Plate=1147 Col=8 Row=M"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                      Score 34.4; DB 13;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                                Mismatches
/organism="Homo sapiens"
/db_xref="taxon:9606"
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37.2%; Score 34.6; DB 10; Length 631;

Query Match

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68 aggattttacagtaataaagaaac

348

q δŏ

AQ743241.1 GI:5520763

DEFINITION

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

RESULT 9 AQ743241/c

Homo sapiens

ORGANISM

REFERENCE AUTHORS

human.

Hood, L

MEDLINE COMMENT

JOURNAL

TITLE

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Darrel medic.
Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 587)
Gyorgyey,J., Vaubert,D., Jimenez-Zurdo,J.I., Charon,C., Troussard
AQ764101 515 bp DNA GSS 28-JUL-1999
HS.2001_Al_G12_MR CIT Approved Human Genomic Sperm Library D Homo
saplens genomic clone Plate=2001 Col=23 Row-M, DNA sequence.
AQ764101
                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 515)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               High Throughput Sequencing Center
University of Washington
University of Washington
University of Washington
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2001 row: M column: 23
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ388941 587 bp mRNA EST 21-MAR-2000
AJ388941 Medicago truncatula R108 Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2001 Col=23 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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Pred. No. 2.7e+02;
0; Mismatches 34;
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61.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 964 row: H column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                 HS_5388_B1_D10_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=964 Col=19 Row=H, DNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 846)
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/db_xxef="fexon:9606"
/clone="Plate=964 Col=19 Row=H"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
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Class: BAC ends

source

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36.6%; 61.1%;

Conservative

RESULT 10 AQ764101

61

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1 Similarity 55; Conserv

Best Loc Matches

Query Match Local

291

BASE COUNT ORIGIN

9

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/clone="263409"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ545066 545 bp DNA GSS 28-MAY-1999
CITBL-E1-263409.TF CITBL-E1 Homo sapiens genomic clone 263409, DNA
sequence.
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
                                                                                     Institut des Sciences Vegetales
Centre National de la Recherche Scientifique (CNRS)
Av. de la Terrasse Bat.23, Gif-sur-Yvette, 91198, FRANCE
Additional information about these EST clones can be downloaded
 ,L., Kondorosi,A. and Kondolosi,E.
Analysis of Medicago truncatula nodule expressed sequence tags
Mol. Plant Microbe Interact. 13 (1), 62-71 (2000)
                                                                                                                                                                                 http://www.cnrs-gif.fr/isv/AK/index.html. (URL provided by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447 AAATTNCAAAATTATTTCATACTTTATTATAATAATATTTCTTAGTTCCTGGTAATCAT 388
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                                                                                                                                                                                                                                                                                                                             /clone_lib="Medicago truncatula R108"
/tissue_type="symbiotic root nodule"
/dev_stage="developing young nodule"
/note="vector: NoLix Lambda HybrizAp"
75 c 99 g 206 t 6 ot:
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Pred. No. 2.9e+02;
0; Mismatches 27;
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Kondorosi, A. and Kondorosi, E.
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AQ545066.1 GI:4903792
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Best Local Similarity 64.5%;
Matches 49; Conservative
                                  Mol. Plant Microbe I
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Contact: Gyorgyey J
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/organism="Homo sapiens" /db_xref="taxon:9606"

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                                                                                  /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
a 96 c 87 g 177 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV739051 CB Homo sapiens cDNA clone CBLAPG08 5', mRNA sequence. AV739051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 ATAGTGAATTATTTTTCCTGAAAATTTTGTCAAAAATAGTCAATAATAGATTGACAATCG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 aaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatca 61
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351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 545;
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Pred. No. 3.6e+02;
0; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.2; DB 13
Pred. No. 3.3e+02;
0; Mismatches 33
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/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 tgtctgaggattttacagtaataaagaaa 90
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9

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VERSION

TITLE

COMMENT

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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Emmail: nelsayed@tigr.cog
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                               TA195A02P 549 bp DNA GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 195a02, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 549)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  1 aaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trýpanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                438 TGTCTTGAGGCTGCTTAGGAAATTTAGAA 466
                                                                                                               61 atgictgaggattitacagtaataaagaa 89
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Job time: 2836 sec
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(bases 1 to 549)
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Best Local Similarity 60.7
Matches 54; Conservative
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TA195A02P/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|qi|ah129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the linsert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 547)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                     AZ648187 547 bp DNA GSS 14-DEC-2000
1M0517001F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0517001 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Vector: PWD42nv: Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/db_xref="taxon:10090"
/clone="UUGC1M0517001"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0517 row: 0 column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 547.
Location/Qualifiers
AZ648187.1 GI:11780403
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Fax: 801 585 7177
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SOURCE
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REATURES

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                                                                                                                            Gaps
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                                                                                                  Length 549;
                                                                                                Score 33; DB 13;
Pred. No. 3.6e+02;
0; Mismatches 35
/organism="Trypanosoma brucei"
                                                 4
                                                 160
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                                                                                                  35.5%;
60.7%;
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Gaps

.. 0

35.5%; Score 33; DB 13; Length 547; 60.7%; Pred. No. 3.6e+02; live 0; Mismatches 35; Indels

54; Conservative

Matches

Query Match Best Local Similarity

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c 12 100.0 39 21 AAA97403 Pea pra2 light-rep . 13 12 100.0 48 21 AAA97396 Pea pra2 light-rep . 14 12 100.0 52 21 AAA97397 Pea pra2 light-rep . 15 12 100.0 53 21 AAA97418 Pea wild-type pra2 . 16 12 100.0 54 21 AAA97417 Pea wild-type pra2 . 17 12 100.0 93 21 AAA97384 Pea pra2 qene liqh	12 100.0 147 16 AAT22540 12 100.0 300 21 AAA01517 12 100.0 344 20 AAV90257 12 100.0 468 22 AAT12374	22 12 100.0 400 22 AA102286 24 12 100.0 646 21 AAC93808 25 12 100.0 651 22 AA106265 25 12 100.0 651 22 AA106265	26 12 100.0 724 22 27 12 100.0 727 21 28 12 100.0 852 22 29 12 100.0 1126 21	12 100.0 1129 20 AAX27340 Human secreted 12 100.0 1138 19 AAV46314 Human secreted 12 100.0 1138 22 AAF98480 Human cDNA clon	33 12 100.0 1188 20 AA252916 Human prostate 34 12 100.0 1221 18 AAV74319 Staphylococcus 35 12 100.0 1279 21 AAC34384 Arabidopsis tha	12 100.0 1341 22 AAC8738 Human secret 12 100.0 1341 22 AAC8738 Arabidopsis 12 100.0 1342 22 AAC8738 Screevisias 12 100.0 1434 20 AAX16007 DNA encoding	41 12 100.0 1405 42 12 100.0 1605 43 12 100.0 1666 44 12 100.0 1677 45 12 100.0 1706	ALIGNMENTS	RESULT 1 AAA97383 ID AAA97383 standard; DNA; 12 BP.	A.C. AAA97383; XX DT 29-JAN-2001 (first entry)	XX DE Pea pra2 gene light-repressible promoter core region. XX KW GTP-binding protein pra2; pea; light-repressible promoter; KW photoinhibitory; expression cassette; transgenic plant; KW deterioration prevention; storage; core region; ds.	XX OS Pisum sativum. XX	21	PF 03-MAR-2000; 2000WO-JP01269. XX DR 12-MAR-1999. 99TP-0066551	(SUNR) SUNTORY	AA PI Sasaki Y, Nagano Y, Inaba T; XX	WPI; 2000-587526/55.	PT New DNA fragment or promoter for expressing a target gene, specifically PT under photoinhibitory conditions, and for transforming a plant cell or PT plant to improve quality and prevent deterioration during storage .
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM nucleic - nucleic search, using sw model	Run on: April 3, 2002, 04:30:10; Search time 189.71 Seconds (without alignments) 54.230 Million cell updates/sec	Title: US-09-700-187-1 Perfect score: 12 Sequence: 1 ggattttacagt 12	table: IDENTITY_NUC Gapop 10.0 ,	Searched: 930621 segs, 428662619 residues Total number of hits satisfying chosen parameters: 1861242	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database: N_Geneseq_1101:* 1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:* 2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:* 3: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:* 4: /SIDS2/gcgdata/geneseqn/NA1983.DAT:* 5: /SIDS2/gcgdata/geneseqn/NA1983.DAT:*	6: /SIDS2/gcgdata/geneseqn/NA1985.DAT:* 7: /SIDS2/gcgdata/geneseqn/NA1986.DAT:* 8: /SIDS2/gcgdata/geneseqn/NA1986.DAT:*	9: \SIDS2/gcgdata/geneseq/geneseqn/NA1988 DAT:* 10: \SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:* 11: \SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:* 12: \SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:* 13: \SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*	14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:* 15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:* 16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*	1/: SIDSZ/Gogdata/geneseg/genesegn/NAL996.DAT:* 18: /SIDSZ/Gogdata/geneseg/genesegn/NAL997.DAT:* 19: /SIDSZ/gogdata/geneseg/genesegn/NAL998.DAT:* 20: /SIDSZ/gogdata/geneseg/genesegn/NAL998.DAT:* 21: /SIDSZ/gogdata/geneseg/genesegn/NAL900.DAT:* 22: /SIDSZ/gogdata/geneseg/genesegn/NAZ000.DAT:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Result Query No. Score Match Length DB ID Description	12 100.0 12 21 12 100.0 22 20 12 100.0 25 20	12 100.0 30 21 AAA97433 12 100.0 31 21 AAA97411	12 100.0 31 21 AAA97412 12 100.0 31 21 AAA97423	31 21 AAA97424 31 21 AAA97427 31 21 AAA97428 31 22 AAI30154

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Sequence 22 BP; 7 A; 7 C; 3 G; 5 T; 0 other;
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02-DEC-1999;
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AAA68434
ID AAA6
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                                                         The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. The present sequence represents the pea pra2 promoter core region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSH6; MutS homologue; plant; DNA mismatch repair; genetic variation; characteristic; microsatellite; primer; PCR; amplification; SSLP; ss; simple sequence length polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12; DB 21; Length 12; Pred. No. 4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 28; 117pp; English.
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Claim 1; Page 17; 49pp; Japanese.
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100.0%;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
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AAX79146/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for identifying a bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a bacteriophage coding region for treating bacterial infections comprises identifying a nucleic acid encoding a product that inhibits bacteria when a bacteriophage infects a bacterium \cdot
                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage; antimicrobial; genome; identification; antibacterial; bacterial growth inhibition; PCR primer; RBS; ribosome biding site; bacterial infection; ss.
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                          Length 22;
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                          100.0%; Score 12; DB 20; 100.0%; Pred. No. 4.1e+02;
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100.0%; Pred. No. 4.1e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage 3A ORF RBS sequence 3AORF180.
                                                                             0; Mismatches
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99US-0407804.
99US-0157218.
99US-0168777.
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Query Match
Best Local Similarity luv...
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nes 12; Conserva
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                                                                                                                                                            Bacteriophage 3A.
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Synthetic.

AAA97393;

AAA97393 RESULT

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and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. Sequences AAA97411-A97412 represent oligonucleotides used in an exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage -
Pea wild-type pra2 gene light-repressible promoter oligonucleotide, WT1
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                                     GTP-binding protein pra2; pea; light-repressible promoter; photoinhibitory; expression cassette; transgenic plant; deterioration prevention; storage; ss.
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ID AAA97412 standard; DNA; 31 BP.
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                Pea pra2 light-repressible promoter mutant LS1 PCR primer, SEQ ID NO:11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage -
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                                                                                                                                                                                                                                                                          GTP-binding protein pra2; pea; light-repressible promoter;
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                                                                                                   AAA97393 standard; DNA; 30 BP.
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10 ggattttacagt 21
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Matches 12; Conserv
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Gaps

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AAA97411

RESULT

Query Match

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under photoinhibitory conditions, and for transforming a plant cell or
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                                                                                                                                                                                     The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. Sequences AAA97411-A97412 represent oligonucleotides used in an exemplification of the invention to generate a wild-type pea pra2 promoter fragment.
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                                                                                                                  New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage -
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100.0%; Pred. No. 4.1e+02;
iive 0; Mismatches 0;
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                                                                      Inaba T;
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 03-MAR-2000; 2000WO-JP01269.
                        99JP-0066551.
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Best Local Similarity 100.
Matches 12; Conservative
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The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. The present sequence represents a wild-type pea pra2 promoter fragment (bases -672 to -642 of the pra2 gene) which comprises the pra2 promoter core region (AAA97383).
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to improve quality and prevent deterioration during storage
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100.0%; Pred. No. 4.1e+02;
tive 0; Mismatches 0;
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                                                                                 Example 7; Fig 6a; 49pp; Japanese.
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Best Local Similarity

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and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. Sequences AAA97424-A97429 represent mutant pea praz promoter fragments (corresponding to bases -672 to -642 of the gene) which comprise the praz promoter core region.
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Query Match

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               Indels
Pred. No. 4.1e+02;
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Best Local Similarity 100.
Matches 12; Conservative
               12; Conservative
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               Matches
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deterioration prevention; storage; PCR primer;
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                             Pisum sativum.
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                                                                                                                                              12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pea pra2 light-repressible promoter clone PL4C PCR primer, SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                  Human; resequence; genotype; disease; forensic; paternity testing;
                                                                                                                                                                                                                     /standard_name= "single nucleotide polymorphism"
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                                                                     Human single nucleotide polymorphism (SNP) PCCB 3.
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hes 0;
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Pred. No. 4.1e+02;
0; Mismatches 0;
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                                                                                                                 nucleotide polymorphism; SNP; ss
                                                                                                                                                                                                                                                                                                                                                                                   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                    Location/Qualifiers
replace(16,A)
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Best Local Similarity 100.0%;
Matches 12; Conservative 0;
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                                       18-OCT-2001
                                                                                                                                              Homo sapiens
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            AAI30154;
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The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression eassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. Sequences AAA97387-A97392 and AAA97398-A97410 represent PCR primers used in an exemplification of the invention to amplify the pea pra2 promoter for cloning.
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                                                                                                                                                                                                                                                                                                                                                                                                     New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 BP; 7 A; 8 C; 7 G; 17 T; 0 other;
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                                                                                                                                                                                                                                              Inaba T;
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03-MAR-2000; 2000WO-JP01269
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RESULT 15
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     \overset{\text{\tiny A}}{\times}\overset{\text{\tiny A}}{\times}\overset{\text{\tiny A}}{\circ}\overset{\text{\tiny A}}{\overset{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}{\overset{\tiny A}}\overset{\text{\tiny A}}}{\overset{\tiny A}}\overset{\text{\tiny A}}\overset{\text{\tiny A}}\overset{\text{\tiny A}}}{\overset{\tiny A}}\overset{\text{\tiny A}}\overset{\text{\tiny A}}\overset{\text{\tiny A}}
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                                                                                                                                                                                                                                                                                                                                                      New DNA fragment or promoter for expressing a target gene, specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                 under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage -
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Matches 12; Conservative
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                                                                           The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. Sequences AAA97391-A97398 represent PCR primers used in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. Sequences AAA97417-A97418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pea wild-type pra2 gene light-repressible promoter oligonucleotide, WT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52 BP; 19 A; 9 C; 12 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Example 3; Page 13; 49pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to mutate the pea pra2 promoter.
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CC represent oligonucleotides used in an exemplification of the invention CC to generate a wild-type pea pra2 promoter fragment.

SQ Sequence 53 BP; 21 A; 11 C; 3 G; 18 T; 0 other;

Query Match

Query Match

Best Local Similarity 100.0%; Score 12; DB 21; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 3, 2002, 05:18:30 Job time: 2900 sec

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nucleic search, using sw model

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3, 2002, 05:13:00

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

US-09-700-187-2 93

Title: Perfect score: Sequence:

Scoring table:

9b_ba:*
9b_htg:*
9b_om:*
9b_om:*
9b_om:*
9b_ph:*
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em_hum:* em_in:*

em_ov:* em_pat:* em_ph:* em_om:* em_or:*

em_ro:* em_pl:* em_sts: em_un:* em_sy:*

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

GenEmbl:*

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Database

length: 0 length: 2000000000

DB seq DB seq

Minimum Maximum

of

Total number

Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_vi:*
em_htgo_hum:*
em_htgo_inv:*
em_htgo_rod:*
em_htg_hum:*
em_htg_inv:*
em_htg_rod:*

em_htg_other:*

SUMMARIES

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assembly was confirmed by restriction digest. The following
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baum, J.A.
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On Apr 21, 2001 this sequence version replaced gi:13443424.
On Apr 21, 2001 this sequence version replaced gi:13443424.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with nis sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempte was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BaA84640.1"
/db_xref="GI:5926718"
/translation="MNQEMNGVEAEKLQEKIDYVFKVVVIGDSAVGKTQILSRFTKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FCFDSKSTIGVEFQTKTVTINGKLIKAQIWDTAGQERYRAVTSAYYRGÅLGAMLVYDI
TKRQTFDHVARWVEELRSHADGSIVIMLIGNKGDLVDQRGVQTEDAVEFAEDQGLFFS
ETSAFSGENVNSAFLKLLQEINKVVSKRSLECNNGIKGNGHDVAALKGEKIDIISAS
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                                                         Graduate
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Nagano,Y.
Direct Submission
Submitted (07-0CT-1997) Yukio Nagano, Nagoya University, Gr
School of Bioagricultural Sciences; Chikusa, Nagoya, Aichi
464-8601, Japan (E-mail:nagano@agr.nagoya-u.ac.jp,
Tel:81-52-789-4168, Fax:81-52-789-4296)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL360267 157381 bp DNA PRI 22-MAY-20
Human DNA sequence from clone RP11-342C20 on chromosome 13,
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join(2326. .2567,2729. .3188)

/gene="pra2"

join(2326. .2567,2729. .3188)

/note="light-repressible GTP binding protein"

/codon_start=1
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100.0%; Pred. No. 1.3e-10;
Live 0; Mismatches 0;
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/db_xref="taxon:3888"
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Direct Submission
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abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw.:, SWISSPROT; Tr., TREMBL; Wp:, WORWPEP; Information on the WORWPEP database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cure 121811. .121816
//orte="Sequence from overlapping clone bA365J7 (AL359472).
Assembly confirmed by restriction digest."
51039 a 27179 c 27761 g 51402 t
                                                                                                                                                                                      Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-342C20 is from the library RPCI-11.2 constructed by the group of Pleter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                                                                                                                                                                           This sequence is the entire insert of clone RPI1-342C20 The true left end of clone RPI1-365J7 is at 99075 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42229 AAAATAACAGACATTTTGATCATTTGTAAATATAAGCTAGATGATAGTAAATGCTACAAA 42170
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Bacillus/Staphylococcus group; Bacillus; Bacillus cereus group.
1 (bases 1 to 2498)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-NOV-1993) Jim A. Baum, Ecogen Inc., Strain Development, Molecular Genetics, 2005 Cabot Boulevard West, Langhorne, PA 19047-1810, USA
Langhorne, PA 19047-1810, USA
L. 2498
/organism="Bacillus thuringiensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64251...64259
/note="Sequence from uni-directional dGTP big dye terminator reads only."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     In5401, a new class II transposable element from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 157381;
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J. Bacteriol. 176 (10), 2835-2845 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.6; D
Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 tgtctgaggattttacagtaataaagaaacga 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="13"
/clone="RP11-342C20"
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Bacillus thuringiensis
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Best Local Similarity 63.03
Matches 58; Conservative
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U03552
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us-09-700-187-2.rge

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/organism="Homo sapiens"
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/clone="RP11-48719"
                                                                                                                                                                                                                                             AL161624.7 GI:14160916
                                                                      288 TTTAAAAGTAATATAAAA 305
                                                    89
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Direct Submission
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                                                                                                                                                         AL161624/c
                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                               ORGANISM
                                                    72
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KEYWORDS
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                                                                                                                                                                                                                                                                               SOURCE
                                                                                   Db
                                                      δy
                                                                                                                                                                                                                                                         /translation="MEVFPIDKDIKEIFCSHLKNNRHQFVENWKNKMIISEKDPFKLE VVQNGEDLLELIIELTMEDKDINYLQPLCEKIAIERAGADANIGDFVYNANVGRNELF
                                                                                                                                                                                                                                                                                            EAMCELDVSARELKPIMAKIHTCFDKLIYYTVLKYSEIISKNLEEKOQYINETHKERL
ILGQMSASEYHBFRNPLTSIMGFVKLLKADHFSLSYIDJISHELDQLMFRISQFLLV
SKIEMWINESRFWHENPLTDILIQFIYPSLYNLIYPIPLYGYRSEVRQYFL
NILMNSIDALESMKERKIIIIVFEEDQAIRTVIKNNGPMIPAENVETIFEPFYTYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1042 AAAATACATACTTGTTTTGACAAATTAATTTATTATACGTTTTAAAAATACTCGGAAATT 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aconophora ferruginea 125 mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aconophora ferruginea.
Mitochondrion Aconophora ferruginea
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 atattttgataaatttattactaaaactattttctagtacttgttaatcatgtctgagga 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-NOV-1996) Exploratory Research, Human Genome Sciences, 9410 Key West Ave., Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
Membracoidea; Membracidae; Aconophora.
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Pred. No. 1.1e+02;
0; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="12S small subunit ribosomal RNA"
25 c 43 g 141 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                  LGTGIGLFVCKQIVEKHNGSIMCRSDNDWTEFQIAFQK"
                                                                                                                                                                                        /evidence-experimental
/product-"histidine protein kinase"
/protein_id-"AAA64586.1"
/db_xref-"GI:520402"

    .340 "Aconophora ferruginea"
/organelle="mitochondrion"
/db_xref="taxon:54606"

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                                                                                                                                                                                                                                                                                                                                                                                    867 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37.2; DE
Pred. No. 56;
0; Mismatches
                                                                                                                                       /codon_start=1
/transl_table=11
/function="phosphorylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sub_species="kurstaki"
/db_xref="taxon:1428"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgtctgaggattttacagtaataaagaaa 90
                                                                                                                     /standard_name="HknA"
                                                                                                                                                                                                                                                                                                                                                                                    444 g
/strain="EG7566"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.18;
66.78;
                                                                    /gene="hknA"
                                                                                   682. .1800
/gene="hknA"
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Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity 63.3
57; Conservative
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Best Local 9
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VERSION

SOURCE

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RESULT

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LOCUS

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During sequence assembly data is compared gi:13274323.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at the world at the world
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RP11-48719 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-21282 is at 13292 in this sequence. The true right end of clone RP11-274M8 is at 100 in this
AL161624 133021 bp DNA PRI 18-MAY-2001
Human DNA sequence from clone RP11-48719 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/ChrX
RP11-48719 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133021)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 982. .1042
/note="MER69 repeat: matches 1. .62 of consensus"
1311. .1622
/note="AllSp repeat: matches 1. .310 of consensus"
2450. .2552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118. .425
/note="AluSq repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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/note="%1.05" repeat: matches 2. 299 of consensus" 17945. 18142
/note="MIR repeat: matches 1. 199 of consensus" /note="MIR repeat: matches 30. 262 of consensus" 18160. 1838
/note="MIR repeat: matches 1. 301 of consensus" 1823. 19345
/note="Aluxg repeat: matches 6010. 6141 of consensus" 19470. 19565
/note="Aluxgy/x repeat: matches 5010. 6141 of consensus" 19470. 19565 102. 9441 note="Tigger3b repeat: matches 887. .1231 of consensus" 1445. .9971 note="Tigger3b repeat: matches 2. .540 of consensus" 1050. .21545 note="Charlielb repeat: matches 14. .523 of consensus" 1800 .14023 Mote-"MER53 repeat: matches 1. .189 of consensus" Mote-"MIR repeat: matches 10. .262 of consensus" Mote-"LIMP3 repeat: matches 6105. .6169 of consensus" 14724. .14834 /note="AluSg/x repeat: matches 137. .310 of consensus" Thote-"AluSq.x repeat: matches 1. .111 of consensus" [4836. .14980]
Note-"MER20 repeat: matches 69. .218 of consensus" [7477. .1510]
Note-"MIR repeat: matches 84. .255 of consensus" [7000. .17310]
Note-"AluSx repeat: matches 1. .312 of consensus" 19571. .19723

/note="L2 repeat: matches 2008. .2143 of consensus"
19724. .20154
/note="ML72FB repeat: matches 3. .414 of consensus"
20155. .20431
/note="L2 repeat: matches 1666. .2008 of consensus"
20458. .20767
/note="ML71C repeat: matches 131. .466 of consensus"
20768. .20931 1662. .21901 note="Alusgi repeat: matches 1. .300 of consensus" 12056. .22620 note="LTR26 repeat: matches 43. .603 of consensus" .2750 of consensus" .2568 of consensus" .2486 of consensus" 7889. 7901 /note="AluSq repeat: matches 1. .313 of consensus" 8993. 9101 /note="MIR repeat: matches 156. .262 of consensus" 7611. .17646 note="MIR repeat: matches 199. .234 of consensus" 7647. .17944 22624. .22930 /note="AluJb repeat: matches 1. .311 of consensus" 22938. .23111 .304 of consensus" .304 of consensus" note="FRAM repeat: matches 0. .163 of consensus" 5104. .5413 /note="AluSp repeat: matches 1. .3 5900. .6018 5900. .6018 /note="L2 repeat: matches 2486. .2 6019. .6316 /note="AluSp repeat: matches 1. .3 6317. .6514 /note="L2 repeat: matches 2187. .2 7589. .7901 repeat: matches 2636. 974. .10116 repeat_region repeat_region

Jabora. Jabora. Amer gtgt 91% conserved" 35365...3535
Anote="MER45 repeat: matches 1...171 of consensus" 3606-366...35667
Anote="MER45 repeat: matches 1...298 of consensus" 4086...47086
Anote="LiPA6 repeat: matches 11...4967 of consensus" 4708-...47086
Anote="LiPA6 repeat: matches 3...299 of consensus" 47087...48267
Anote="LiPA6 repeat: matches 3...299 of consensus" 48774...48803
Anote="LiPA6 repeat: matches 4967...6141 of consensus" 48774...48803
Anote="LiPA6 repeat: matches 905...934 of consensus" 49784...48813
Anote="Alux repeat: matches 57...309 of consensus" 49863...50116
Anote="Alux repeat: matches 1...183 of consensus" 50156...50344
Anote="MER44 repeat: matches 1...183 of consensus" 50342...50612
Anote="MER44 repeat: matches 421...728 of consensus" 51509...51638 /note="MIR repeat: matches 50, .262 of consensus" 54482. .54616
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; 0

Indels

26; DB 9;

Score 36.4; DB Pred. No. 49; 0; Mismatches

Query Match 39.1%; Best Local Similarity 66.7%; Matches 52; Conservative

; 0

Length 133021;

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39.1%; Score 36.4; DB 2; Length 169671; 66.7%; Pred. No. 48; ive 0; Mismatches 26; Indels 0;
                                           1: gap of unknown length
7: contig of 8525 bp in length
7: gap of unknown length
8: contig of 8796 bp in length
8: gap of unknown length
8: contig of 11860 bp in length
8: contig of 11879 bp in length
9: contig of 15279 bp in length
9: contig of 15279 bp in length
9: gap of unknown length
9: contig of 17764 bp in length
9: contig of 14764 bp in length
9: contig of 14723 bp in length
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7: gap of unknown length
9: contig of 14723 bp in length
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9: contig of 25034 bp in length
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32782. 41939
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42040. 48802
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/51. .8768
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144638 . 169671
/note="assembly_name:Contig24"
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   of 9158
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/db_xref="taxon:9606"
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                            AC021098 169671 bp DNA HTG 01-SEP-2000
Homo sapiens chromosome X clone RP11-33A2, WORKING DRAFT SEQUENCE,
18 unordered pieces.
                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 169671)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mar 13, 2000 this sequence version replaced gi:6922906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13: 81%
Sequencing vector: plasmid; 19%
Sequencing vector: plasmid; 19%
Chemistry: Dye-primer ET: 81% of reads
Chemistry: Dye-terminator Big Dye; 19% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 159126 bases at least 030
Consensus quality: 162659 bases at least 020
Insert size: 170000; agarose-fp
Insert size: 170000; agarose-fp
Ouality coverage: 4.16 in 020 bases; sum-of-contigs
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Center code: WUGSC
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Waterston, R.H.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Smith,D.R.
Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
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/clone="RP11-244B22"
/clone=lib="RPCI human BAC library 11"
a 31409 c 30665 g 38092 t 2598 others
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Best Local Similarity 67.6%; Pred. No. 72;
Matches 50; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary Statistics
Consensus quality: 103103 bases at least Q40
Consensus quality: 114063 bases at least Q20
Consensus quality: 114063 bases at least Q20
Consensus quality: 120184 bases at least Q20
Estimated insert size: 115300; agarose-fp estimation
Estimated insert size: 138879; sum-of-contigs estimation
Quality coverage: 4.08 in Q20 bases; agarose-fp estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 25 contigs. The true corder of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 141279)
DOE Joint Genome Institute.
4 agtaacacatattttgataaatttattactaaaactattttctagtacttgttaatcatg 63
                                                                                                                                                                                   Homo sapiens chromosome 16 clone RP11-244B22, WORKING DRAFT SEQUENCE, 25 unordered pieces.
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gap of unknown length
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                                                                                                                                                                                                                                AC023824.3 GI:13786370
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN.
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gap of unknown
                                                                                                                                                                                                                                                                                                                                                          Sequencing of Human Chromosome 16
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
Center Project Name: 0
Center clone name: RPCI-11_244B22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.jgi.doe.gov
                                                                           141279 bp
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KEYWORDS
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24; Indels

Length 141279;

us-09-700-187-2.rge

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51071 a 29071 c 26776 g 48019 t
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AC027071/c
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Submitted (21-JUL-2001) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On Jul 21, 2001 His sequence version replaced gi:13605969.
Location/Qualifiers
1. 154937
             Direct Submission
Submitted (19-OCT-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
3 (bases 1 to 142654)
Smith, D.R.
                                                                                                                                                                                               Submitted (12-OCT-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA on May 2, 2000 this sequence version replaced gi:6862698.

Location/Qualifiers
1. .142654
                                                                                                               Submitted (02-MAY-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA 4 (bases 1 to 142654) Smith,D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-FEB-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA (bases 1 to 154937)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC022537 154937 bp DNA PRI 21-JUL-2001 Homo sapiens chromosome 10 clone RP11-40C11, complete sequence. AC022537
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154937)
Smith,D.R.
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Pred. No. 72;
0; Mismatches
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46421 a 27094 c 25546 g 43593
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                                                                                                                                                                                                                                                                                 /organism="Homo sapiens'/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 atgtctgaggattttacagtaataaagaaa 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-40C11"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                       /chromosome="10"
/clone="RP11-76F22"
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Best Local Similarity 62.2%;
Matches 56; Conservative
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AL Uppublished

Surren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Glande, S., Goyette, M., Graham, L., Hawler, J., Lancorque, K., Landers, T., Lehoczky, J., Hevine, J., Larocque, K., Landers, T., Lehoczky, J., Klein, J., Larocque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Maddonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, M., McRennan, K., Meneus, L., Minova, T., Maranda, C., Mlenga, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollara, Y., Rajmond, C., Riley, R., Rogov, P., Rothman, D., Stanger-Inhaman, N., Stojanovic, N., Subramanian, A., Tatayliao, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Voung, G., Zahouor, J., Zimmer, A. and Zody, M.

Submitted (27-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker: html
http://ftp.genome.washington.edu/RM/Repeatmasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50143)
                                                                                                                                                                                         Db 87539 AAAAATTAAAACCCATGTTACTTTTTCAAGTACTAAAAAATAGTTTTATAGTCAATC 87598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACO27071 50143 bp DNA HTG 27-MAR-2000 Homo sapiens chromosome 9 clone RP11-200D20 map 9, LOW-PASS SEQUENCE SAMPLING.
                                                                               Gaps
                                                                                                                                                   1 aaaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc 60
   Length 154937;
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: £7662
                                                                               Indels
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                                                                           34;
Score 35.6; DB 9;
Pred. No. 71;
0; Mismatches 34;
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HTG; HTGS_PHASE0.
   Query Match 38.3%;
Best Local Similarity 62.2%;
Matches 56; Conservative
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                           will be sequenced to completion. In the event that the record is updated, the accession number will
and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 bp
f 765 bp in length
100 bp
f 801 bp in length
                                                                                                             of 100 bp
contig of 782 bp in length
                                                                                                                                     of 100 bp contig of 761 bp in length of 100 bp
                                                                                                                                                                                                                                                                                    100 bp
f 791 bp in length
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784 bp in length
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100 bp
788 bp in length
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765 bp in length
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0472 11254: contig of 783 bp in length
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805 bp in length
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781 bp in length
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795 bp in length
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28085: contig of 778 bp in length
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798 bp i
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772 bp
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12131: contig of 777 bp
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18356 18455: gap of
18456 19220: contig of 765
19221 19320: gap of
19221 20121: contig of 80
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14011: contig of 78

14001: gap of 100

215096: contig of 70

715796: gap of 10
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136: gap of 10
13917: contig of 7
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18355; contig of 1
18455; gap of 1
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26342: contig of
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27207: contig of
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2530: con
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39542: contig of 794 bp in length
42: gap of 100 bp
40428: contig of 786 bp in length
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99: gap of 100 bp

46588: contig of 789 bp in length

88: gap of 100 bp

47479: contig of 791 bp in length

779: gap of 100 bp
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40529 41296: contig of 768 bp
41297 41396: gap of 100 bp
41397 42178: contig of 782 bp
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contig of 788 bp
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38648: contig of 784 bp
48: gap of 100 bp
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44812; contig of 773 bp
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17580 48358; contig of 779 bp
                         gap of 100 bp
16: contig of 788 bp
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Pred. No. 90;
0; Mismatches
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/clone_lib="RPCI-11 Human
a 11483 c 11252 g 10779
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/db_xref="taxon:9606"
/chromosome="9"
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contig of

us-09-700-187-2.rge

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AC009130/c
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AUTHORS
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Unpublished

E (bases 1 to 175691)

ES Bruce, D., Mundk, M., Dogett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.

Biratted (20-MAY-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA

On Jul 3, 2001 this sequence version replaced gi:13928651.

Sequence Quality Assessment:
This entry has been annotated with sequence quality

This entry has been annotated with sequence quality
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                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                clone RP11-528K16, WORKING DRAFT
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/clone="RP11-528K16"
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0; Mismatches
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                                                                                           EQUENCE, 1 ordered pieces.
                                                                Homo sapiens chromosome 16
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DOE Joint Genome Institute.
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Consensus quality: 158339 bases at least Q40
Consensus quality: 17631 bases at least Q30
Consensus quality: 180631 bases at least Q30
Consensus quality: 180631 bases at least Q30
Estimated insert size: 187296; sum-of-contigs estimation
Quality coverage: 3.4 in Q20 bases; agarose fp estimation
Quality coverage: 3.6 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 43 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 21, 2000 this sequence version replaced gi:7689948.
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191496)
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16 clone RP11-501P17, WORKING DRAFT
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contig of 1102 b
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Sequencing of Human Chromosome 16
Unpublished
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Center clone name: RPCI-11_501P17
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Center Code: JGI
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                                                                                                                                          Homo sapiens chromosome 16 closeQUENCE, 43 unordered pieces
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Page 10

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contig of 14443 bp in length
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/chromosome="16"
/cloone="RP11-501P17"
/clone=lib="RPCI human BAC library 11"
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FEATURES Source

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Consensus quality: 193032 bases at least Q40
Consensus quality: 199717 bases at least Q30
Consensus quality: 199717 bases at least Q30
Consensus quality: 202073 bases at least Q30
Consensus quality: 222073 bases at least Q30
Consensus quality: 222073 bases at least Q30
Estimated insert size: 239000; agarose-fp estimation
Estimated insert size: 239000; agarose-fp estimation
Quality coverage: 6.8 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.6 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a "working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
truns of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Pr 25, 2001 this sequence version replaced gi:9954601.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                             26;
                                                                                     DB 2;
47031 a 47510 c 47005 g 45732 t
                                                                                  Score 35.4; DB Pred. No. 76; 0; Mismatches
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Center Code: JGI
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/strain="LA 716"
/db_xref="taxon:28526"
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D 110362 ATAGTAGCTCATATTTTGTTAAATTTATCCCTAAGAATTTTATGATTCACTTGCAAATGG 110303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paracentromeric sequences on tomato chromosome 6 show homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Joacovez 2 (bases 1 to 721), Weide,R., Koornneef,M. and Zabel,P. Weide,R., Hontelez,J., van Kammen,A., Koornneef,M. and Zabel,P. Direct Submission
Submitted (19-JUN-1998) Phytopathology, Wageningen Agricultural Iniversity, Binnenhaven 9, Wageningen 6709 PD, The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 721)
Welde,R., Hontelez,J., van Kammen,A., Koornneef,M. and Zabel,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF072528 721 bp DNA PLN 29-SEP-1998
Lycopersicon pennellii clone AG15 paracentromeric sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human satellite III and to the mammalian CENP-B binding box Mol. Gen. Genet. 259 (2), 190-197 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 210043;
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53123 a 52905 c 51736 g 50777 t 1502 others
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Best Local Similarity 66.2:
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CEBU 15A, UK. Familia equilibres; nunquery@sanger.ac.uk Clone requests; clonerequest@sanger.ac.uk

On Aug 21, 2000 this sequence version replaced gi:9843543.

During sequence assembly data is comparaded from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw: SWISSRORT: Tr:, TREMBL: Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGY/Chr20

IMPORTANT: This sequence is not the entire insert of clone RP5-93HH9 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP5-1187M17 is at 35737 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequencing problems, such as compressions and repeats; all regions were otherwise noted: all regions were either double-stranded or sequencing problems, such as compressions and repeats; all regions were objection by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. RP5-93HH9 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/Dacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL160414 35836 bp DNA PRI 15-FEB-2001
Human DNA sequence from clone RP5-931H19 on chromosome 20. Contains
ESTS. GSSs and CpG islands. Contains the OXT gene for oxytocin
(neurophysin I) and the AVP gene for arginine vasopressin
(neurophysin II), complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 35836)
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Submitted (13-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; AVP; CpG island; neurophysin; OXT; oxytocin; vasopressin.
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/chromosome="6"
/map="centromere"
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d	135836	/organism="Homo sapiens" /db_xref="texon:9606" /rhromosome="10"	/clone="Romo"		<pre>/note="AluY repeat: matches 1158 of consensus" 21422408</pre>	/note="AluSx repeat: matches 1296 of consensus" 28.4 31.2	/note="Jusx repeat: matches 1290 of consensus"	of 5005 of 500	555/38/0 /note="AluJb repeat: matches 1307 of consensus"	416/441/ /note="MIR repeat: matches 40262 of consensus"	44194/23 /note="AluSp repeat: matches 1312 of consensus" // End	45545240 //note=-Alusp repeat: matches 3298 of consensus"	ozez3393 footemark repeat: matches 1310 of consensus"	53943704 /note="LiMC4 repeat: matches 77017813 of consensus" 5765 50A	Jobs3394 Jobe="FLAM_C repeat: matches I133 of consensus"	5905. 5242 //octe="LiMASA repeat: matches 5478. 5827 of consensus"	oz430340 /rote=-Alusx repeat: matches 18309 of consensus"	00310079 /note="L1M4 repeat: matches 26982746 of consensus"	6/01/023 //note="match: GSS: Em:AQ318472"	6/017051 /note="match: GSS: Em:AQ782226"	<pre>67217033 /note="AluSp repeat: matches 1313 of consensus" </pre>	<pre>complement(70327218) /note="match: GSS: Em:A0236587 Em:A0239242"</pre>		complement(70347218)		/note="match: GSS: Em:AQ614522" complement(70457218)	/note="match: GSS: Em:AQ545857" 70487220	/note="match: GSS: Em:AQ044844" 72337297	/note="LIM1 repeat: matches 11901252 of consensus"		//orte="AluJo repeat: matches 6307 of consensus"	/015//98 /note="LIM1 repeat: matches 9981190 of consensus"	/800/932 /note="AluSq/x repeat: matches 1133 of consensus"	/93/80/4 /note="Alusg repeat: matches 1140 of consensus"	80758382 /note="AluYa5 repeat: matches 5311 of consensus"	83838550 /note="AluSq repeat: matches 140302 of consensus"	87309040 /note="AluJb repeat: matches*2312 of consensus"		
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//note="L2 repeat: matches 1881. .2104 of consensus"
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19440. .19473
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                                                                                                                                  Query Match 37.6%; Score 35; DB 9; Length 35836; Best Local Similarity 70.1%; Pred. No. 1.1e+02; Matches 47; Conservative 0; Mismatches 20; Indels (
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Qy 73 tttacag 79 || | | | Db 14655 TTCTCGG 14649

Search completed: April 3, 2002, 05:14:06 Job time: 4161 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

April 3, 2002, 05:14:51; Search time 81.95 Seconds (without alignments) 257.016 Million cell updates/sec Run on:

US-09-700-187-2 93 1 aaaagtaacacatattttga......ttacagtaataaagaaacga 93 Title: Perfect score: Sequence:

Scoring table:

351203 seqs, 113238999 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched:

702406

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPIFS

					SUMMARIES	
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Result No.	Score	Query Match	Length	DB	ID	Description
0	29.4	31.6	1984	-4	US-07-885-970A-25	Sequence 25, Appl
0	29.4	31.6	1985	7	US-08-298-687A-25	25,
3	29.4	•	1985	П	US-08-298-829-25	25,
4	29.4	31.6	6373	3	US-08-462-728-1	1, 1
5	29.4	31.6	6375	7	US-08-168-917-5	'n
9	29.4	31,6	6375	7	US-08-460-510-5	'n
7	29.4	31.6	6375	7	US-08-460-490-5	'n
80	29.4	31.6	6375	Ŋ	PCT-US92-00730-5	Sequence 5, Appli
6	29.4	31.6	6375	S	PCT-US92-00862-5	Ŋ,
10	28.2	30.3	392	4	US-09-385-982-95	95,
	28.2	30.3	4576	П	US-08-832-883-49	49,
7	28.2	30.3	4576	~	US-08-832-877-49	49,
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Н	28.3	30.3	4673	Ŋ	PCT-US92-00018-1	'n
c 15	28.2	30.3	6138	4	US-09-067-800-4	4,
c 16	28.2	30.3	6138	4	US-09-349-677-4	4
	28	30.1	2290	9	5312912-1	23
18	27.6		1947	m	US-08-604-991-1	Sequence 1, Appli
19	27.6		1947	٣	US-09-363-639-1	'n
20	27.4		617	7	US-09-385-982-222	22
21	27.4	29.5	296	4	US-08-960-780-47	47
22	27.4	29.5	296	4	US-09-073-898-47	
23	27.2	29.2	713	4	US-08-998-416-956	926
c 24	27.2	29.5	3974	4	US-08-467-504-3	
25	27.2	29.5	5336	4	•	17
26	27.2	29.5	6471	4	US-09-353-585-1	Sequence 1, Appli
c 27	27	29.0	3095	9	5231168-1	Patent No. 5231168

2, Appli 807, App	779, App	289, App	l, Appli	3, Appli	105, App	-	-	_	1036, Ap	172, App	224, App	535, App	538, App
Sequence 8	Sequence	Sequence			Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sednence	Sequence	Sednence
US-09-316-083-2 US-09-328-111-807	US-08-998-416-779	US-08-998-410-1130 US-08-998-416-289 US-08-958-642-3	US-08-778-394-1	US-08-778-423A-3	US-08-687-080-105	US-08-998-416-185	US-08-998-416-701	US-08-998-416-683	US-08-998-416-1036	US-08-998-416-472	US-08-998-416-224	US-08-998-416-535	US-08-998-416-538
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26.8 26.6	26.6	26.6	26.6	26.6	26.6	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4
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TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
                                                                                                               36;
                                                                         31.6%; Score 29.4; DB 1;
58.6%; Pred. No. 8.1;
iive 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
COUNTRY: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 07/253,243
APPLICATION NUMBER: US 07/253,243
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholass J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 221-5139
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC COMPETIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,687A
                                                                                                                                                                                                                                                                  963 AGGCTTAAATTTCAACCGATAATAAAG 937
                                                                                                                                                                                                                              61 atgtctgaggattttacagtaataaag 87
                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-298-687A-25/C
Sequence 25, Application US/08298687A
Patent No. 5521078
GENERAL INFORMATION:
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ORCANISM: Gossypium barbadense
STRAIN: Sea Island
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1985 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                     Query Match
Best Local Similarity 58.69
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL-SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
; CLONE: SIH6
US-07-885-970A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 53701
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31.6%; Score 29.4; DB 1; Length 1985;

Query Match

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                            Gaps
                                                               1 aaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc 60
                                                                                                          1023 AAAATTATAATTTAATATTATAAAACCATTAATAATAAATTATATTTTAAGGTCTTGCTGTAA 964
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                          36; Indels
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3
3(2)-08-292-25/c
5(2)-08-298-29
5 Patent No. 5620882
6 GENERAL INFORMATION:
7 TITLE OF INVENTION:
7 TITLE OF INVENTION:
7 TITLE OF SEQUENCES:
7 TITLE OF SEQUENCES:
7 TITLE OF SEQUENCES:
7 TOWER OF SEQUENCES:
7 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
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Pred. No. 8.1;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
    Pred. No. 8.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/29,829
FILING DATE: 19-CCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/5,970
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US/07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US/07/617,239
FILING DATE: 04-CCT-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                           963 AGGCTTAAATTTCAACCGATAATAAAG 937
                                                                                                                                                  61 atgtctgaggattttacagtaataaag 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
TELEPHONE: (608) 283-2478
TELEPAS: (608) 251-5139
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.6%;
Best Local Similarity 58.6%;
Matches 51; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1985 base pairs
Best Local Similarity 58.6%
Matches 51; Conservative
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EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: Sea Island IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Madison
STATE: Wisconsin
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY:
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APPLICANT: Fretto, Larry J.
APPLICANT: Giese, Neill A.
APPLICANT: Escobedo, Jaime A.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is identical to the nucleotide number 1 of the previous 4100\ \mathrm{long}\ \mathrm{sequence}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6029 AGTTATACATATACATATACATAAAGATATATCTGAACCTCTTATGACGTTTTGTAAATACTG 6088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note= "nucleotide number 1 of this
                                                                                                                                                                                                                                                                                                             ADDRESSE: TOWNSEND and TOWNSEND STREET: Steuart Street Tower, 20th Floor \ One Market STREET: Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/650,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12418-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET NUMBER: 1241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 36-2400
                                       Sequence 5, Application US/08168917
Patent No. 5686572
                                                                                                        APPLICANT: Wolf, David APPLICANT: Tomlinson, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 6375 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo Sapiens
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Best Local Similarity 58.6
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: lambda qti0
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US-08-168-917-5
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                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                               94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                      US-08-168-917-5
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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1 aaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc 60
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                                                                                                                                                                                                                                                                                           APPLICANT: WILLIAMS, Lewis T.
APPLICANT: ESCOBEDO, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
UNMER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6373;
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                                                                                                                                                                                                                                                                                                                                                                                                                            One Market, Steuart Street Tower, 20th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/462,728 FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                     Townsend and Townsend and Crew
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Pred. No. 8.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/309,322
FILING DATE: 10-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6087 ITCGACATAGTGACGGAAGCAAATATA 6113
                                                                                                                         963 AGGCTTAAATTTCAACCGATAATAAAG 937
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                                                                                 61 atgtctgaggattttacagtaataaag 87
                                                                                                                                                                                                           US-08-462-728-1
; Sequence 1, Application US/08462728
; Patent No. 6043211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Dow, Karen B. REGISTRATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
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58.6%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6373 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.69
Best Local Similarity 58.69
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                STREET: ONE MAINCE.
CITY: San Francisco
GTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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STRANDEDNESS:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                    RESULT 7
US-08-460-490-5
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                     APPLICANT: Wolf, David
APPLICANT: Tomlinson, James E.
APPLICANT: Tomlinson, James E.
APPLICANT: Fretto, Larry J.
APPLICANT: Giese, Neill A.
APPLICANT: Giese, Neill A.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6029 AGTTATACATATACATAAAAAAAATATCTGAACCTCTTATGACGTTTTGTAAATACTG 6088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "nucleotide number 1 of this offHER INFORMATION: sequence is identical to the nucleotide number OTHER INFORMATION: of the previous 4100 long sequence" US-08-460-510-5
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                                                                                                                                                                                                                                                                                                    STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              012418-001430
6089 TTCGACATAGTGACGGAAGCAAATATA 6115
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02-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 01241
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 326-2400
TELEFAX: (415) 326-2402
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6375 base pairs
                                                                                           Sequence 5, Application US/08460510 Patent No. 5872218
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MOLECULE TYPE: cDNA to mRNA
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo Sapiens
STRAIN: lambda gt10
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Best Local Similarity 58.6
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 129..3395
                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 02 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       94105
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                                                                                                                                                                                                                                                                                        E: TOWNSEND and TOWNSEND and CREW One Market Plaza, Steuart Street Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/460,490 FILING DATE: U2-JUN-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29.4; DB Pred. No. 8.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29,684
ER: 012418-001420
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Sequence 5, Application US/08460490;
Patent No. 5891652;
GENERAL INFORMATION:
APPLICANT: Wolf, David
APPLICANT: Tomlinson, James E.
APPLICANT: Fretto, Larry J.
APPLICANT: Giese, Neill A.
APPLICANT: Bscobedo, Jaime A.
APPLICANT: Williams, Lewis T.
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 29,684
REPERENCE/DOCKET UNDHER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SED ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.6%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 6375 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
STRAIN: lambda gtl0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.6'
Matches 51; Conservative
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
                                                                                                                                                                                                                                                                                                                                   San Francisco
California
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LOCATION: 129
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6029 AGTIATACATATACATAAAGATATATCTGAACCTCTTATGACGGTTTTGTAAATACTG 6088
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                    APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
UNMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "nucleotide number 1 of this sequence is identical to the nucleotide number 1 of the previous 4100 long sequence."
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58.6%; Pred. No. 8.9;
iive 0; Mismatches 36; Indels C
                                                                                                                            ADDRESSEE: TOWNSEND and TOWNSEND STREET: Steuart Street Tower, 20th Floor CITY: San Francisco STATE: California COUNTRY: US
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00862
FILING DATE: 19920131
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/151,141
FILING DATE: 02-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/309,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 tctgaggattttacagtaataaagaaa 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 23071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6375 base pairs
                                                                                                                                                                                                                                       ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-FEB-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 129..339
OTHER INFORMATION:
OTHER INFORMATION:
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  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-09-385-982-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                         APPLICANT: Wolf, David
APPLICANT: Tomlinson, James E.
APPLICANT: Fretto, Larry J.
APPLICANT: Glese, Naill A.
APPLICANT: Glese, Naill A.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /note= "nucleotide number 1 of this profile is of the nucleotide number 1 of the nucleotide number 1 of the nucleotide number 1 of the previous 4100 long sequence" pcr-us92-00730-5
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                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSEND and TOWNSEND
STREET: Streart Street Tower, 20th Floor \ One Market
STREET: Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00730
FILING DATE: 19920128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6089 TTCGACATAGTGACGGAAGCAAATATA 6115
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                Sequence 5, Application PC/TUS9200730 GENERAL INFORMATION:
APPLICANT: Wolf, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application PC/TUS9200862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 12418
TELECOMMUNICATION INFORMATION:
TELEFRAN: (415) 326-2400
TELEFRAN: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6375 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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58.6%;
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Best Local Similarity 58.6
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1992012
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                    94105
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PCT-US92-00862-5
PCT-US92-00730-5
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Gaps

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INFORMATION FOR SEQ ID NO:
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Patent No. 5807681
CENERAL INFORMATION:
APPLICANT: Giordano, Antonio
APPLICANT: Baldi, Alphonso
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
TITLE OF INVENTION: OF CANCER
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.3%; Score 28.2; DB 4; Length 392; 54.8%; Pred. No. 15; tive 0; Mismatches '42; Indels
Patent No. 6262334
GENERAL INFORMATION:
FAPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
                                                                                                         TILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER PELLOR NUMBER: 60/117,393
EARLIER PELLOR APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 95
LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 atgtctgaggattttacagtaataaagaaacga 93
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NAME: MORACO, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US1
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : NAME/KEY: misc_feature

: LOCATION: (1)...(392)

: OTHER INFORMATION: n = A,T,C or G

US-09-385-982-95
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 54.8
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: PA
COUNTRY: US.
ZIP: 19102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 116
                                                                                                                                                                                                                      .
,
                                                                                                                                                                              Length 4576;
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                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,877
                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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ilarity 61.6%; Pred. No. 18;
Conservative 0; Mismatches
                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                Score 28.2;
Pred. No. 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 49, Application US/08832877; Patent No. 5840506; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-08-832-877-49
                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-832-883-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEO ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              Query Match 30.3%;
Best Local Similarity 61.6%;
Matches 45; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 4576 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4576 base pairs
                                            TYPE: nucleic acid
STRANDEDNESS: double
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3417 TAGTTATTTATA 3405
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        66 tgaggattttaca 78
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Best Local Similarity
Matches 45; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-08-832-877-49/c
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GENERAL.

GENERAL.

APPLICANT: Hoffman, Step.c...

APPLICANT: Charoenvit, Yupin

APPLICANT: Hedstrom, Richard

APPLICANT: Hostrom, Richard

APPLICANT: Rogers IV, William O.

TITLE OF INVENTION: Immunogen and gene encoding

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: A David Spewack

STREET: Medical Center

STREET: Medical Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 aaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: Py-lambdagt11-2-7 kb genomic expression CLONE: Py10.1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Plasmodium yoelii
STRAIN: 17X(NL)
DEVELOPMENTAL STAGE: erythrocytic stage
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                         4154 ATGAAAGAGAATAATAATATTAAAAAAA 4126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00018
FILING DATE: 19920103
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 atgtctgaggattttacagtaataaagaa 89
    61 atgtctgaggattttacagtaataaagaa
                                                                                                                                         Sequence 1, Application PC/TUS9200018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SPEWAGE, AVTAM D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4673 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erythrocytic stage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 718..3195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 718.31
COTHER INFORMATION:
PCT-US92-00018-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 51; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20814-5044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: N
ORIGINAL SOURCE:
                                                                                                     RESULT 14
PCT-US92-00018-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                       Dp
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                                                                                                                                                                                                                APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria sporozoite surface protein
TITLE OF INVENTION: immunogen and gene
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                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: A. David Spevack
STREET: NMRDC Building 1 T-12 National Naval
STREET: Medical Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28.2; | Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythrocytic stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:

AUGURENT APPLICATION DATA:

APPLICATION NUMBER: US/07/638,431 FILING DATE: 19910110

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Spewack, Avrom D.

TELECOMMUNICATION INFORMATION:

TELEFAX: (301) 295-679

TELEFAX: (301) 295-4033

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4673 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS; double
                                                                                                                                   Sequence 1, Application US/07638431
Patent No. 5198535
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE: erythrocytic stage
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                                                                                                                                                                                                 Hoffman, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Plasmodium yoelii
STRAIN: 17X(NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.3%;
ilarity 57.3%;
Conservative
                                   3417 TAGTTATTTATA 3405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE:
TISSUE TYPE: Blood
66 tgaggattttaca 78
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cli.
STATE: ML
COUNTRY: USA
The 20814-5044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 718.31
; OTHER INFORMATION:
US-07-638-431-1
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Best Local Similarity
Matches 51; Conserv
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ORIGINAL SOURCE:
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NAME/KEY: misc_feature
LOCATION: 1.6138
COTHER INFORMATION: /label- AGL5_promoter
HTFORMATION: /note- "Nucleotide sequence of the AGL5 promoter."
US-09-067-800-4
                                                                                          GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Yanofsky, Martin F.
APPLICANT: Ferrandiz, Cristine
TITLE OF INVENTION: Seed Dispersal
TITLE OF INVENTION: Seed Dispersal
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
CITY: San Diego
COMPUTR: United States
TIP: 93.122
COMPUTR: Floppy disk
COMPUTR: IN PC Compatible
COMPUTER: READABLE FORM:
MEDIUM TYPE: POPDY disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31, 815
REFERENCE/DOCKET NUMBER: 9-UD 2948
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPRAXION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6138 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
FEATURE:
                                                 Sequence 4, Application US/09067800 Patent No. 6198024
RESULT 15
US-09-067-800-4/c
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ó: Gaps ; Query Match 30.3%; Score 28.2; DB 4; Length 6138; Best Local Similarity 57.3%; Pred. No. 18; Matches 51; Conservative 0; Mismatches 38; Indels 0

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63 gtctgaggattttacagtaataaagaaac 91

3316 ACCTAATGATCAATCTGCAGAAATAAAAC 3288

Search completed: April 3, 2002, 05:14:55 Job time: 3905 sec

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Genomic fragment # Plasmodium falcipa

DNA sequence encod 50 kD subunit of S Staphylococcus aur

Staphylococcus aur Chromosome 13q31-q

Arabidopsis thalia Arabidopsis thalia Cotton fibre-speci Cotton fibre clone

DNA encoding a Sta

Cotton H6 gene and 2099 bp Candida al Type A human plate

BAC containing rep Mycoplasma genital Borrelia burgdorfe

Human colon cancer

New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage -

under plant

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Score

Result . ₽ WPI; 2000-587526/55.

Perfect score:

Sequence:

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Run

Scoring table:

Searched:

DB DB

Minimum Maximum ..

Database

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GTP-binding protein pra2; pea; light-repressible promoter; photoinhibitory; expression cassette; transgenic plant; deterioration prevention; storage; cis element; ds.
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                           The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. The present sequence represents the pea pra2 promoter cis element.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. The present sequence
cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is starticularly useful for agricultural products. The present sequence represents the pea pra2 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1396 aaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc 1455
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                                                                                                                                                                                                                                                                                                                                                                                                  1 aaaagtaacacatattttgataaatttattactaaaactattttctagtacttgttaatc
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                                                                                                                                                                                                                                                                   Length 2325;
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                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                Sequence 2325 BP; 791 A; 451 C; 317 G; 766 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pea light-repressible GTP-binding protein pra2 cDNA.
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                                                                                                                                                                                                                                                                Score 93; DB 21;
Pred. No. 2.8e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA97382 standard; cDNA; 3441
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUNR ) SUNTORY LTD.
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    93;
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Query Match

Best Local

Matches

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                        Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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Pred. No. 6.1;
69; Mismatches
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                    BP.
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3.3%;
AAF58254/c
ID AAF58254 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
                                                                              (first entry)
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                                                                                                          Oligonucleotide D1875
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Best Local Similarity
Matches 3; Conserva
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                                                                          Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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 100.0%; Score 93; DB 21; Length 3441; 100.0%; Pred. No. 2.8e-14;
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                                                                                                                     Mismatches
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Pred. No. 6.1;
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3.3%; E
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Best Local Similarity 3.3%;
3; Conservative
                               Conservative
                                                                                                                                                                                                                                                                                                                        Oligonucleotide D1835
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              Similarity
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26-JUL-1999;

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                         present invention relates to a composition comprising two nucleic
                                                                                                                                                                                                                                                                                                                                                                                                     acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                         DB 22;
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3.3%; F
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                  monitoring gene expression
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                                                                                                                                                                                                                                                                                                                                         3; Conservative
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Best Local Similarity
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                                                    a single surface
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Pred. No. 6.1;
69; Mismatches 18;
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                                                                                                                                                                                                                                                                Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
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Best Local Similarity 3.3%;
Matches 3; Conservative 6
                                                                 2000WO-US20476
                                                                                                    99US-0145695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              monitoring gene expression
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Oligonucleotide D2004

24-APR-2001

AAF58259;

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õ 셤 ò g gene expression; ss

WO200107665-A2

Synthetic.

01-FEB-2001

26-JUL-1999;

WPI; 2001-159728/16

Umek RM;

AAV21210

RESULT

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                                                                Indels
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Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
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                                      DB 22;
                                   ; Score 33.6; Di
Pred. No. 6.1;
69; Mismatches
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Pred. No. 6.1;
59; Mismatches
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                                                                                                                                           61 atgtctgaggattttacagtaataaagaaa 90
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3.3%; 1
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ilarity 3.3%; E
Conservative 69
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17-MAR-2000; 2000US-0190259.
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                                                               Conservative
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                                     Query Match
Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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The present sequence represents the large circular extrachromosomal element sequence of the Methanococcus jannaschii circular chromosome. The present invention describes M. jannaschii open reading frames from the genome sequence. The invention also describes a computer based system for identifying fragments of the M. jannaschii genome that are homologous to target nucleotide sequences, comprising; (a) data storage means comprising the nucleotide sequence of the 1664976, 58407 or 16550 bp sequence (see AAV21209, AAV21210 and AAV21211), or a nucleotide sequence of the nucleotide sequence of the data storage means to identify a homologous sequence, and (c) retrieval means for comparing a target sequence to the nucleotide sequence of the data storage means to identify a homologous sequence, and (c) retrieval means for obtaining the homologous sequence. The method, which is based on whole genome random sequencing of an autotrophic archaeon M. jannaschii, the genome of which consists of 3 physically distinct elements, a large circular chromosome (the 1664976 bp sequence given in AAV21209), a large circular extra chromosomal element (the 58407) bp sequence given in AAV21211), and a small circular extra chromosomal element (the identification of M. jannaschii genome frammat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii; methanogenic archaeon; circular chromosome; genome; autotrophic; extrachromosomal element; identification; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of methano-genic archaeon, Methanoccoccus jannaschii - useful in identification of M. jannaschii genome
                                                                                                              Methanococcus jannaschii large circular extrachromosomal element.
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65.8%; Pred. No. 9;
ive 0; Mismatches 25; Indels
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(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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AAV21210 standard; DNA; 58407 BP.
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Best Local Similarity 65.8%
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                                   AAV21210;
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RESULT 11

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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17-MAR-2000; 2000US-0190259
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17-MAR-2000; 2000US-0190259.
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Best Local Similarity
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                                            WO200107665-A2.
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               Synthetic.
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1.1%; Pred. No. 9.3;
ive 71; Mismatches 18;
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                                                            AAF58238 standard; DNA; 244 BP
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17-MAR-2000; 2000US-0190259
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monitoring gene expression
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                                                         Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                  The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
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                                                                                                                                                                                                                                                             Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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   Pred. No. 9.5;
71; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 atgtctgaggattttacagtaataaagaaa 90
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                                                                                                                        Example 6; Page 127; 159pp; English.
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1.1%; F
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17-MAR-2000; 2000US-0190259.
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Umek RM;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                        Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
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Best Local Similarity 1.1%; Pred. No. 9.5;
Matches 1; Conservative 71; Mismatches
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                         AAF58262
AAF58255
AAAF58238
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AAY0151
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      RESULT
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1 aagctttaaaggcaagggaa......tttttgatcttgacaagaaa 2325
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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AAF58254
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                                      The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants ir which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. The present sequence
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New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage -
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Query Match

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d. No. 5.7e-29;
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Pred.
Best Local Similarity 0.6%; Pred
Matches 5; Conservative 552;
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552; Mismatches
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17-MAR-2000; 2000US-0190259
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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ve 552; Mismatches 230;
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            (CLIN-) CLINICAL MICRO SENSORS INC.
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                                                                                                                                                                                                                                                                                                                                             Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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Conservative 548; Mismatches
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                                                                                              and single-nucleotide polymorphisms, e.g. for genotyping monitoring gene expression.
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                                                                                                                                 Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other
                                                                                                                                                                   8.5%; Score 197.6; DB 0.6%; Pred. No. 7.4e-29; Live 548; Mismatches 22
                      Example 6; Page 127; 159pp; English.
                                                                                                                                                                                             Conservative 548;
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Matches 5; Conserv
single surface
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RESULT 11 AAF58257

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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0.6%; Pred. No. 7.4e-29;
7ative 548; Mismatches 227;
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936
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17-MAR-2000; 2000US-0190259.
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AAF58257 standard; DNA;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                          Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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Example 6; Page 128; 159pp; English.
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17-MAR-2000; 2000US-0190259
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DB 22;
           larity 0.6%, Pred. No. 7.4e-29;
Conservative 548; Mismatches 22
Score 197.6;
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Matches 5, Conserv
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2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monitoring gene expression.
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                            AAF58255 standard; DNA;
                                                                                                                                                                                                                                         Oligonucleotide D1876.
                                                                                                                                                                                                                                                                       gene expression; ss
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Best Local Similarity
Matches 5; Conserv
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                     Query Match

8.5%; Score 197.6; DB 22;
Best Local Similarity 0.6%; Pred. No. 7.4e-29;
Matches 5; Conservative 548; Mismatches 227;
                                                                                                                                                     Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
                                                                                                                                                                                              Example 6; Page 128; 159pp; English
                                                                                          (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...
                                                           99US-0145695.
2000US-0190259.
                                       26-JUL-2000; 2000WO-US20476
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                                                                                                                                 WPI; 2001-159728/16
                                                                                                                                                                            single surface
WO200107665-A2.
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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.4e-29;
nes 227; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Electron-transfer group; ETM; mismatch; genotyping;
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Pred. No. 7.4e-2
18; Mismatches
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WPI; 2000-587526/55.

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3, 2002, 05:19:04

completed: April

Search completed: Job time: 2934 sec

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New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage -
                                                                                                                                                                 The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression cassette of the invention can be used to generate transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. The present sequence represents the pea pra2 promoter cis element.
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Matches: 93; Conserv
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Length 19124;
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COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Bear
16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50.4;
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45
ANDRESS:
Cabe Martens Olson & BerET: 620 Newport Center Drive ''.
Newport Beach
7: California
9: California
9: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/487,826B
                                                                                                                                                                                                                                                                     Sequence 13, Application US/08487826B Patent No. 5993827 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NH1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 10-SEP-1993
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CITY: Ne
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  (without alignments)
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Sequence 185
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Sequence 33,
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                      Compugen Ltd.
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US-08-973-462-1
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US-08-25-11231-1
US-08-99-953-2
US-08-416-534
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           GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Match
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43.6
43.2
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Query Match
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APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALANIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TITLE OF INVENTION: MALANIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT APPLICATION NUMBER: US/08/973,462B
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER PFILING DATE: 1996-06-13
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                18154 ATTTATAATACAATATTATATATAGTTTCCTATTAAAATTAAATTAATATATACAATAAT 18213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18094 TGTTACTCTAATTCTGAATAATCCGAGCGAAAAAAAATTATATAATCTCATATAAAAATT 18153
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                                                                                                                          tgtttatcccttgcacacatttcacatcaatttattaaaaacattttaccattggaaaaca 1890
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                                                 Gaps
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Pred. No. 0.031;
0; Mismatches 248; Indels 1
                                             Indels
48.0%; Pred. No. 0.038;
Live 0; Mismatches 156;
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Best Local Similarity 45.89
Matches 210; Conservative
                                        Matches 144; Conservative
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; ORGANISM: P. falciparum
US-08-973-462-1
Best Local Similarity
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                                                                     aactetattaacaceggtaatteaacaacegttgttgttgtegagtteatgttttetteeaae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carmen Rodriguez, Paralegal, Arnold, White & Durkee
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REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: 33,928
TELECOMUNICATION INFORMATION:
TELEPHONE: (713) 789-2679
INFORMATION FOR SEQ ID NO: 7:
SECTION SECTION OF SEC
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                                                                                                                                                              2229 tottttccttttcctttactttatttatttctcctactt 2267
                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08705937
Patent No. 5981841
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SANTINO. COlleen G.
APPLICANT: Conner. Timothy W.
TITLE OF INVENTION: EARLY SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Janelle D. Waack.
REGISTRATION NUMBER: 36,300
REFERENCE/DOCKET NUMBER: MOI
NAME: Barbara S. Kitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Nicolas G. Barzoukas.
REGISTRATION NUMBER: 38,823
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; MOLECULE TYPE: DNA (genomic)
US-08-705-937-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                 US-08-705-937-7/c
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APPLICATION NUMBER: US/08/299,953 FILING DATE: Herewith
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-
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CLASSICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2182 ccggtaattcaaca 2195
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                                                                                                                                                                                        Sequence 33, Application US/08772440
Sequence 33, Application US/08772440
Sequence 33, Application US/08772440
Setent No. 6046158
GENERAL INFORMATION:
APPLICANT: Aritzumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEROF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: Elappy disk
COMPUTER: DEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: CONCURRENTLY HEREWITH
FILING DATE: CONCURRENTLY HEREWITH
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OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "D = A or G or
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LOCATION: 3564..7896
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "M = A or C"
FEATURE:
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LOCATION: 3479..6422
OTHER INVEMENTION: /mod_base= OTHER
OTHER INFORMATION: /mote= "R = A or G"
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OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "K = G or
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
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NAME: Parker, David L.
REGIESTRATION NUMBER: 32,165
REFRENCE/DOCKET NUMBER: UTXD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                            646 TATAAATAACAAGTAAAATAAA 625
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 10409 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY: modified_base
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OTHER INFORMATION: //
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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1945 tagaatattttgtaattatagcacaattttcaaaaatatcctagtcttcaacc---actc 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
NAME/KEY: modified_base
LOCATION: 3405..6871
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mote= "S = C or G"
FEATURE:
NAME/KEY: modified_base
LOCATION: 3457..9998
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mod_base= OTHER
FEATURE:
                                                                                                                                                                                             NAME/KEY: modified_base
LOCATION: 3595. 9999
COTHER INFORMATION: /mod_base= OTHER
US-08-772-440-33
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Expression of Foreign Proteins to the Plant Epidermis
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                                                        E: Woodcock Washburn Kurtz Mackiewicz & No. 5744334ris
One Liberty Place 46th. Floor
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                                                                                                            STATE: PA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 359;
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Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                               NOVA-0003
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/459,415
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                             FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/299,953
                                                                                                                                                                                                                                                                                                                                                                                                            34,293
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: NC TELECOMMUNICATION: TELEPHONE: 215-564-8960
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ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2861 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                            Philadelphia
     FITLE OF INVENTION:
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                                                            ADDRESSEE:
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US-08-459-415-1
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                                                                                                                                                                                                                                                                                                               Length 2861;
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                                                                                                                                                                                                                                                                                                                   DB 1;
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Pred. No. 0.
                    NOVA-0003
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Patent No. 5744334
GENERAL INFORMATION:
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: NOVA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-564-8960
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     ...cology: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
AWTI-SENOT
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                                                                                                                             LENGTH: 2861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                              Best Local Similarity 44.1
Matches 289; Conservative
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US-08-299-953-1
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APPLICANT: Dobres, Michael S. and Mandaci, Sevnur
TITLE OF INVENTION: A Plant Promoter Useful for Directing the
TITLE OF INVENTION: Expression of Foreign Proteins to the Plant Epidermis
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  797 AATACTGGCATATCACCATTATTACTAACATGTCATTAAAAATAAGATTTAAAAAAGTAA 856
                                                                                                                                                                                                    917 ATTGAATACTAGCTTTTATGGCACTCCAATTAGTTTGACACATTGAATACTAGCTTTCAT 976
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & No. 5646333ris
STREET: One Liberty Place 46th. Floor
                                                                    agaataacctccgcaacatcaaagtcagaaacctcttgtaactcttcagttgaaacgaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/299,953 FILING DATE: Herewith
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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REFERENCE/DOCKET NUMBER: NOV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-564-896
TELEFAX: 215-564-839
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ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3881 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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STATE: PA
The 19103
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9511231
GENERAL INFORMATION:
APPLICANT: Dobres, Michael S. and Mandaci, Sevnur
TITLE OF INVENTION: A Plant Promoter Useful for Directing the Expression
TITLE OF INVENTION: of Foreign Proteins to the Plant Epidermis
1037 CATATGATAATACTCCCTATCATTTTTTATTATGGTTGTTTTGAAAAAAATTATATCAT 1096
                                                                                    94 ttccaaaaacacatcaaagttatgtgattcatatctttaattatctgataatataatt 153
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                                           tatactccaccaagattgctttacatctaaccaagttaatgaatttaaattcttcgaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place 46th. Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 359;
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Pred. No. 0.25;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/299,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: September 2, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,293
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET UNMBER: NOV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-564-8960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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CITY: Philadelphia
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Best Local Similarity
Matches 289; Conserv
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PCT-US95-11231-1
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Plant Epidermis
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5744334ris
STREET: One Liberty Place 46th. Floor
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                                                                                          Length 3881;
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APPLICANT: Dobres, Michael S. and Mandaci, Sevnur
TITLE OF INVENTION: A Plant Promoter Useful for Directing
TITLE OF INVENTION: Expression of Foreign Proteins to the
                                                                                                                      0; Mismatches 359; Indels
                                                                                        DB 1;
                                                                                                        Pred. No. 0.27
                                                                                        2.0%; Score 45.6; 44.1%; Pred. No. 0.
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Patent No. 5744334
 DNA (genomic)
                                                                                                                     Matches 289; Conservative
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MOLECULE TYPE:
HYPOTHETICAL:
                          ; ANTI-SENSE:
US-08-299-953-2
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US-08-459-415-2
                                                                                        Query Match
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1: Floppy disk
IBM PC compatible

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp

19103

STATE:

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ctcatatatttttaagtaataatacccacttcaagtttttttgtttttgttgttgttgtgcag 453
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                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.27;
Mismatches
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                                                                                                                                                                                                                                            NOVA-0003
  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,415
FILING DATE: 02-JUN-1995
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     APPLICATION NUMBER: 08/299,953 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: NO
                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-564-8960
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3881 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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      334 cttcctttacaatttatactctaaggaaatacattagacactctagatgggttgcattag 393
                                        917 ATTGAATACTAGCTTTTATGGCACTCCAATTAGTTTGACACATTGAATACTAGCTTTCAT 976
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APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44.6; DB 1; Length 731;
Pred. No. 0.28;
0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: THE WEBB LAW FIRM STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: PITTSBURGH
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
219-1818
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK
COMPUTER: Widwest Micro 486-50
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/451,405A FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-451-405A-2/c; Sequence 2, Application US/08451405A; Patent No. 5736358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07/965,273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 49.4*
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
FILING DATE: 15-JAN-19
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNKNOWN
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                                                                                                                                                     APPLICANT: Dobres, Michael S. and Mandaci, Sevnur
TITLE OF INVENTION: A Plant Promoter Useful for Directing the Expression
TITLE OF INVENTION: of Foreign Proteins to the Plant Epidermis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtatattcaatatttcatacaattgtgttatatatgaaatattttgtaggtaaagggacta 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agaataacctccgcaacatcaaagtcagaaacctcttgtaactcttcagttgaaacgaga 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATACTGGCATATCACCATTATTACTAACATGTCATTAAAAATAAGATTTAAAAAAGTAA 856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45.6; DB 5; Length 3881;
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                OFFIGURE STATEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: NOVA-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-564-8960
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FLILOSCOPTION CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/299,953
FILLING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
                                                                                                                Sequence 2, Application PC/TUS9511231 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 289; Conserv
                                                                                                                                                                                                                                                                                CITY: F. STATE: PA 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
PCT-US95-11231-2
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360 aaatacattagacactctagatgggttgcattagctcatatttttaagtaataatacc 419
                                                                                                                                                    300 gttcccccacttaacttcttggtttgggtgaggacttcctttacaatttatactctaagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: POLIMENT, Rainer APPLICANT: Steiner Sabine APPLICANT: Steiner Sabine APPLICANT: Mohr Christine APPLICANT: Mohr Christine APPLICANT: Mendland, Jurgen APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENOMIC DNA SEQUENCITILE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                  Sequence 534, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 854 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.9
Best Local Similarity 51.5
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 919-541-868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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US-08-998-416-534
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US-08-998-416-534
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446 AAATAAAAAATTAAAATTTTAAACCTTTGTAAGATAATAGAGTGTGTTAAAAGTGTGT 387
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                                                                                 gttatatgaaatattttgtaggtaaaagggactaagaataacctccgcaacatcaaagtc
                                                                                                                         2206 tegagiteatgittetteetaactetitteetitteetitaettiattiattiet 2260
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT:
MARTIA, Frank N.
TITLE OF INVENTION: Biocontrol of Fungal Soilborne Pathogens
TITLE OF INVENTION: by Pythium oligandrum
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                 Length 1183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,722
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9%; Score 44.2; DB 2; ilarity 40.7%; Pred. No. 0.4; Conservative 0; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                           Sequence 8, Application US/08731722
Patent No. 5961971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
. REPRENCE/POCKET NUMBER: UF-1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
| HOLYUDUAL ISOLATE: 30-1
US-08-731-722-8
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TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: FL
COUNTRY: US
ZIP: 32606-6669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Matches 155; Conserv
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                                                                                                                                                                                                                                 RESULT 12
US-08-731-722-8
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4152 TAATAGGTTCTTAAGATGAATACATATATATATGTTGATTATAATTTATTATTGTTGTATA 4093
1755 tcactggtcaatcactggtcaatgtgttttctcttcccatgaattcacattgctaaagaa 1814
                                                                                                                                                                  1875 ttaccattggaaaacacatacattcaatcaattattttgcattttcaaaaactaaac 1934
                                                                                                                                                                                                                                                 caaacaa--acttagaatattttgtaattatagcacaattttcaaaaatatcctagtctt 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4212 TATCCTTTTACACATTCTTATGTTATTATAAAAAGGAACCAGTTGTTACTATATTG 4153
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                                      4507 TTATTCTTAAAATACTTTTAAATATATATATATAAATTAAATATAGAAATATCTTAATTA
                                                                               1815 aattaccaccttaaaaatgtttatcccttgcacacatttcacatcaatttattaaaaacatt
                                                                                                       1993 caaccactcaataattcacaatttccaaatcccttgcaaaacatcacaacctctagaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris STREET: One Liberty Place 46th Floor STATE: Philadelphia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tatgatataatatgatgcagcaatacacttaatttggtaaagcattaaagcgagacaact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/867,106 FILING DATE: 19920625
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/07867106
Patent No. 5389526
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IBM PC compatible
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REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RIT
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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ADDRESSEE: Woodcock
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US-07-867-106-2
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APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: AND PLASMODIUM FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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                                                          1318 aaaaattcacccaaacaaatgagagagacactacatctctcttattattattaataaaatg 1377
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                                                                                                                                                                    Score 44; DB 2; Length 19124;
Pred. No. 0.93;
); Mismatches 310; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NR/Andersoften Piling Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
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10-SEP-1993
10-SEP-1993
10-SEP-1993
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GENERAL INFORMATION:
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TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
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ilarity 44.8%;
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MEDIUM TYPE: Floppy of
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ADDRESSEE: Knobbe Ma
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STATE: California
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Best Local Similarity
Matches 257; Conserv
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HYPOTHETICAL:
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| TELEFAX: 215-568-3439 |
| INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 5852 base pairs |
| TYPE: NUCLEIC ACID |
| STRANDEDNESS: single |
| TOPOLOGY: linear |
| MOLECULE TYPE: DNA (genomic) |
| ANTI-SENSE: NO |
| FEATURE: |
| NAME/KEY: CDS |
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GenCore version 4.5 'Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

April 3, 2002, 04:39:16; Search time 2120.21 Seconds

(without alignments)
11783.708 Million cell updates/sec

US-09-700-187-3 2325 1 aagctttaaaggcaagggaa......tttttgatcttgacaagaaa 2325

Perfect score:

Sedneuce:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

11351937 seqs, 5372889281 residues Searched:

22703874 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

EST:* Database :

gb_est1:* gb_est2:* gb_htc:* gb_gss:* em_gss_fun:* em_gss_hum:* em_gss_rod:* em_gss_inv:* em_gss_pln:* em_gss_pro:* em_esthum: *
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em_estpl: *
em_estro: *
em_estro: * : em_estfun:* em_htc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_vrt:* em_gss_other:*

SUMMARIES

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Description	AL0639	AL0787	AL0697	AL0619:	AL1088	AL0697	AW7749	AL0659	AL5475	AL0718	AL0694	AI,0694
ID	CNS0039G	CNSOOLT2	CNSOOEVL	CNS00213	CNS0182P	CNSOOEVL	AW774987	CNS006TE	AL547503	CNSOODKY	CNS00E07	CNSOOEPO
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Query Match Length DB ID	1101	1101	1101	1101	1101	1101	587	1101	1125	928	1101	1101
Query Match	3.9	3.9	3.4	3.3	3.2	3.1	3.1	3.0	3.0	3.0	3.0	3.0
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ALIGNMENTS

When I wave, genoscope.cns.fr When I wave, genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC Clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08KLO of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL063921 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101) fruit fly. Drosophila melanogaster AL063921.1 GI:4941778 VERSION KEYWORDS SOURCE ORGANISM DEFINITION TITLE RESULT CNS0039G ACCESSION AUTHORS REFERENCE COMMENT LOCUS

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FEATURES

BASE COUNT ORIGIN

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Muscomorpha; Ephydroidea; Drosophila
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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- web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucyo Oscogawa and Aaron Mammoser in Pieter de Jons's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers Direct Submission Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr 2239 1700 tcaatttaattgtatcgtaaatggtaggacatactcatgctacacaattatatcatcact 1759 1760 ggtcaatcactggtcaatgtgtttttctcttcccatgaattcacattgctaaagaaaatta 1819 ccaccttaaaatgtttatcccttgcacacatttcacatcaatttattaaaacattttacc 1879 1880 attggaaaacacatacatattcaatcaattatttttgcattttcaaaaactaaaccaaac 1939 1940 aaacttagaatattttgtaattatagcacaattttcaaaaatatcctagtcttcaaccac 1999 700 820 260 463 994 HMMMMMMMATTHAWHTTTHTTTYYMMMCMTTHTMMMMMMMMMMMMMMMMMC 935 Gaps 2000 tcaataattcacaatttccaaatcccttgcaaaacatcacaacctctagaaactttgatt 934 СИМИМССССМСМИМИМОММІТІТІННИМССМСМСССМСМСМИМИМАСМИМИМІТІТ aataatctaataaaagcaataatatgatatctaaacaatatcaccatatatgttatgata caccggtaattcaacaaccgttgttgtcgagttcatgttttcttccaactctttccttt taatatgatgcagcaatacacttaatttggtaaagcattaaagcgagacaactctattaa .; 8 Length 1101; 406 others Query Match 3.9%; Score 91; DB 13; Length 11 Best Local Similarity 28.2%; Pred. No. 6.2e-05; Matches 174; Conservative 180; Mismatches 255; Indels /organism="Drosophila melanogaster" /db_xxef="texon:7227" /clone_lib="RPCI-98" /clone="BACR48PI9" 522 2180 g

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isogenic strain y2; cn bw sp, the same strain used for the BDGP's

Pl and EST libraries. A more detailed description of the library

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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Fituery (Dros BAC) was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
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                                                                                                                                                                                       1958
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                                                               tgttttctcttcccatgaattcacattgctaaagaaaattaccaccttaaaatgtttatc 1838
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                                                                                                                                                                                                                                                                                                                                                                                                                                    2139 acttaatttggtaaagcattaaagcgagacaactctattaacaccggtaattcaacaacc 2198
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                                                                                                                                                                                                                                                                                 646 AWAAAAAAWAWTWTTTAAAAWTTTTTTTTTWWTTAWATTAAAAWTAAAWTWTTTAT
                                                                                                                                                                                                                                                                                                                                            2019 aaatcccttgcaaaacatcacaacctctagaaactttgattaataataataaaaagcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
   Length 1101;
                                   Indels

    1101
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"

3.3%; Score 75.6; DB 13;
llarity 42.2%; Pred. No. 0.014;
Conservative 36; Mismatches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fruit fly.
Plasmid Drosophila melanogaster
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                   Similarity
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                               227;
    Query Match
                    Local
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CNS0182P/c
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                        Length 1101;
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                                                                                                                                                          DB 13;
0.025;
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                                                                                                                                                                                              Conservative 204; Mismatches
                                                                              73
                                                                                                                                                        Score 74;
Pred. No.
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN37D10"
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KEYWORDS
SOURCE
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melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial cost digestion of Drosophila DNA provided by the BDCP from the isogenic strain y2: on bw sp, the same strain used for the BDCP's PI and EST libraries. A more detailed description of the library filters for hybridization from the BACP Kesource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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http://www.fruitfly.org The BDGP Drosophila
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                                                                                                                                                                                                                                                                                                                             others
                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29523"
                                                                                                                                                                                                                                                                                                                           232
                                                                                                                                                                                                                                                                                                                                                                                               Score 72.4; DB 13;
Pred. No. 0.044;
i; Mismatches 329;
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                                                                                                                                                                                                                                                                                                                           299
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14; Conservative 116;
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Anotes Vector: pBluescript SK : Site_1: BcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap RN vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

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                                                                                                                                                                                        Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
                                                                                                                                                                                                                                                                                                                                                                                  ESTs from roots of Medicago truncatula after Rhizobium inoculation Unpublished (1999)
                                                                                                                                                                                                                                                                                                                         Ellis, I.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium meliloti"
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                                      587 bp mRNA EST 07-SEP-2000
Medicago truncatula cDNA clone pKV3-25121, mRNA
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                                                                                                                                                                                                                                                                                  1 (bases 1 to 587)
Vandenbosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.
Fraser,C.M.
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Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
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/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kate@mail.bio.tamu.edu
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/clone_lib="KV3"
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                                                                                                                            GI:7718904
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Texas A&M University
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Matches 104; Conservative
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RRCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed describin of the library
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                                                                                                                                                                                                                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                    Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14L09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                          03-JUN-1999
                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Weoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db.xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14L09"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
tttaattgtatcgtaaatggtaggacatactcatgctacacaattatatcatcactggtc 1763
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AL547503 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI011YB03 5
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                              820 ATANTVTRIMIVIAAWATAAATRIMIAMBABRNWWATATAKHKTAGTDWTATHRIRTR
                                                                                                                                                                                                                                   1824 cttaaaaatgtttatcccttgcacacatttcacatcaatttattaaaaacattttaccattg
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43.0%; Pred. No. 0.083;
tive 28; Mismatches 231;
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/db_xref="taxon:9606"
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of prosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BACR29P01 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL069440
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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     191 others
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33.5%; Pred. No. 0.11;
*'ve 78; Mismatches 160; Indels
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/db_xref="taxon:7227"
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Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Straitute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail ; segref@genoscope.cns.fr
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Genoscope

REFERENCE AUTHORS

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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila malanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC infarry was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1.98 and was constructed by partial Concer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1.98 and was constructed by partial ESORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillters for hybridization from the BACPAC Resource Center can be location at http://bacpac.med.ubfalo.edu/drosophila_bac.htm.
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3ACN14L05 of DrosBAC library from Drosophila melanogaster (fruit
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                                                                        fruit fly.
Plasmid Drosophila melanogaster
 fly), genomic survey sequence. AL105604
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/note="end : T7"
                                           AL105604.1 GI:5617618
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                                                                                                                                                                   AUTHORS
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                                                                     Submitted (23 JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded un Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
wascomocpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1204)
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                                                                                                                                                                                                                                                                                                                                                                 others
                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                               312
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Web: www.genoscope.cns.fr)
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                                                                                                                                                                               Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1061)
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/plasmid="pBelobAC11"
/db_xref="taxon:7227"
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Direct Submission

L Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:
2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:
5 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                    CNSOGQXV 759 bp DNA GSS 05-JUL-2001
T7 end of clone AW0AA009H09 of library AW0AA from strain CLIB 89 of
Yarrowia lipolytica, genomic survey sequence.
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Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.

1 (bases 1 to 759)
Casaregola, Neurogalise, C., Lepingle, A., Bon, E., Feynerol, C., Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
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Best Local Similarity 38.7%; Pred. No. 0.17;
Matches 163; Conservative 60; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Yarrowia lipolytica"
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//db_xref="taxon.4952"
/clone="AW0A09H09"
/clone_lib="AW0AA"
/note="end : T7"
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AL411257.1 GI:12180512
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Yarrowia lipolytica
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Search completed: April Job time: 2854 sec

us-09-700-187-1.rst

100.0 172 10 AI029683 100.0 173 13 A2818519 100.0 187 13 A0985182 100.0 180 11 BF235518 100.0 184 10 AV054690	100.0 185 10 AV071084 100.0 185 10 BB357868 100.0 185 11 BG942699 100.0 186 10 AT345298	100.0 190 10 AV288772 100.0 193 10 AV288178 100.0 194 10 A136924 100.0 202 11 D60959 100.0 207 10 A1572468 100.0 210 10 AV336005 100.0 216 13 B29087	100.0 217 10 A1563911 100.0 220 13 A0278868 100.0 223 10 BE236298 100.0 224 10 BE236293 100.0 224 10 BE5144 100.0 225 10 BE55670	12 100.0 226 11 B1220740 B1220740 602938853 12 100.0 227 11 B1293223 B1293223 A129692 zn91e04.s	ALIGNMENTS 1 A 2925237 88 bp DNA GSS 01-APR-2001 N 4910-e222x18.s1 Saccharomyces paradoxus N17 Saccharomyces paradoxus genomic clone 4910.e232x18.s1, DNA sequence. N A2925237 A2925237.1 GI:13496136 GSS. Saccharomyces paradoxus.	ORGANISM Saccharomyces paradoxus ORGANISM Saccharomyces paradoxus Reparyota: Fundi; Ascomycota: Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. 1 (bases 1 to 88) AUTHORS Cliften, P. P. Hillier, L. W., Fulton, L., Graves, T., Miner, T., Gish W.R., Waterston, R.H. and Johnston, M. R. Graves, T., Miner, T., Gish Comparative DNA sequence analysis COMMENT Contact: Johnston M Department of Genetics Washington University Medical School Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA	Tel: 314 362 7835 Fax: 314 362 7855 Email: mj@genetics.wustl.edu Class: random plasmid subclone. Location/Qualifiers 188 /organism="Saccharomyces paradoxus" /strain="N17" /db_taxon:27291" /clone="4910.ez32x18.s1" /clone="taxon:27291" /cl
c 13 14 c 15 16 17	c 18 c 20 c 21 c 22		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. 0 . 0 . 0 . 0 . 0 . 0 . 0 . 0 . 0 . 0	RESULT 1 A292537/C LOCUS DEFINITION ACCESSION KEYMONDS SOURCE SOURCE	ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOUIC
4.5 Compugen Ltd.	Search time 2120.21 Seconds (without alignments) 60.819 Million cell updates/sec	•	1937 seqs, 5372889281 residues satisfying chosen parameters: 22703874 :: 0 :: 200000000		, \	results predicted by chance to have a look the score of the result being printed, of the total score distribution. SUMMARIES ID	A292527 4910.ez32 AW217731 EST266445 A2289196 RPCI-23-5 A1610647 P4D20d2.x BEL45737 IL5-HT020 D25785 HUMGSO4153 AA779315 nf36e06.s AU1080504 AU180504 AQ009485 CIT-HSP-2 AV333933 AV333933 BF881282 QV1-ET018 BF909645 PM3-UT005

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van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Liang
'F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning
'C.M., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A£289196 126 bp DNA GSS 27-JUL-2000
RPCI-23-59823.TJB RPCI-23 Mus musculus genomic clone RPCI-23-59823,
AZ289196
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBlueScript SK(-); Site_1: EcoR1: Site_2: Xhol: supplier: Tanksley: Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
                                                                                         Gaps
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EST296445 tomato flower buds 8 mm to pre-anthesis, Cornell
University Lycopersicon esculentum cDNA clone cTOC6E5, mRNA
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                   Length 88;
                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="flower"
/dev_stage="buds 8mm-to-preanthesis"
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/cultivar="TA496"
                                                   Score 12; DB 13;
Pred. No. 7.3e+03;
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                                                                                     Mismatches
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/clone="cTOC6E5"
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                                                                                  12; Conservative
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                                                                                                                                         40 GGATTTTACAGT 29
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     tomato.
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/note="Organ: Kidney/Brain: Vector: pBACe3.6; Site_1:
CooR: Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
10 c 30 g 38 t
                                                                                                                                                                                                 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Standetign.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jone
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalla: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (Jases 1 to 130)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                     Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 12; DB 13;
100.0%; Pred. No. 7.1e+03;
ive 0; Mismatches 0;
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/clone="RPCI-23-59B23"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Female"
/lab_host="DH10B"
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A2289196.1 GI:9530982
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                                                                                         Mus musculus
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                                                           house mouse
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AI610647/c
LOCUS
DEFINITION
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Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=LL5-HT0207-231 099-006-A01&t3=1999-10-23&t4=1) Seq primer: put forward High quality sequence start: 56 High quality sequence stop: 147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Okubo,K., Itoh,K., Yoshii,J., Yokouchi,H. and Matsubara,K.
Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 147)
Okubo,K., Yoshii,J., Yokouchi,H., Kameyama,M. and Matsubara,K.
Global analysis of gene expression in colon mucosa: a large scale
random cDNA sequencing analysis
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D25785 147 bp .mRNA EST 30-N(V-1995 HUMGS04153 Human colon mucosa Homo sapiens cDNA clone cm1984 3′,
                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone_lib="HT0207"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: pucl8; Site_l: Smal;
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/note="Adult male, tissue_type = colon mucosa
24 c 34 g 26 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 12; DB 10; Length 147; 100.0%; Pred. No. 7e+03;
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35 c 12 g 69 t
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Location/Qualifiers
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                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="cm1984"
                                                                                                                                             Location/Qualiflers
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                                                        Email: cgapbs.remail.nl.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 149-011"
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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LL5-HT0207-231099-006-A01 HT0207 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone~*IMAGE:2188323"
/clone_lib~"NCI_CGAP_Gas4"
/fissue_type~*poorly_differentiated_adenocarcinoma_with
signet_ring_cell_features"
/lab_host-*DH108"
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                        Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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E 1 (bases 1 to 152)
Sanaka, E., Hori, H., Naruse, K., Mitani, H. and Tanaka, M.
Medaka EST analysis
Unpublished (2001)
Contact: Emi Sanaka
Department of Biological Sciences
Graduate School of Science, Nagoya University
Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan
Tel: 81-52-789-2973
Fax: 81-52-789-2974
Email: sanaka@bio.nagoya-u.ac.jp
This clone was isolated from Medaka eye cDNA library (SNK01) 5'end.
Location/Qualifiers
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CIT-HSP-2283N16.TRB CIT-HSP HOMO Sapiens genomic clone 2283N16, UNA
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10.5e of a random BAC End Sequence Database for Sequence-Ready Map Building (1999)
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterrygii; Neopterrygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterrygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Medaka eye cUNA library (SNKOl)"
/tissue_type="eye"
/dev_stage="adult"
/note="Wild samples from Okayama Pref.(Southern part of
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Other GSSs: CIT-RSP-2283N16.TFB
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208

    152
/organism="Oryzias latipes"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="wild type"
/db_xref="taxon:8090"
/clone="NGY10.02c"
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                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 578 Std Error: 0.00
Seq primer: -40ml3 fwd ET from Amersham
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AU180504 Medaka eye cDNA library (SNK01) Oryzias latipes cDNA clone
NGY10.02c, mRNA sequence.
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                                                       AA579315 150 bp mRNA EST 12-SEP-1997 nf36e06.sl NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:915874, mRNA
                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 150)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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/db_xref="taxon:9606"
/clone="ImAGE:915874"
/clone_lib="NCI_CGAP_Pr2"
/sex-"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="45 years old"
/lab_host="DH10B"
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Location/Qualifiers
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                                                                                                                           AA579315
AA579315.1 GI:2357499
                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
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AA579315/C
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Location/Qualifiers
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BF881282.1 GI:12271408
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                                                                                                                                                                                                            /sex="male"
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Best Local Similarity 100.
Matches 12; Conservative
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Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukudas, S., Rusakas, T., Hayatsu, N., Hiozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, K., Shibata, K., Shibata, Y., Shipaka, Y., Suzuki, H., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh.M., Kitsunai.T., Akiyama,J., Shibata,K., Izawa,M., Kawai.J., Tomatu.Y., Carninci,P., Shibata,Y., Muramatsu.M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Wiki.http://genome-gsc.riken.go.jp,
Sasaki, N., Izawa.M., watahiki.M., uzawa.K., Tanaka.T., Yoneda.Y.,
Marsuura.S., Carninci,P., Muramatsu.M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV333933 RIKEN full-length enriched, adult male medulla oblongata Mus musculus cDNA clone 6330552F17 3' similar to X04070 Rat liver
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1999
                                                                                                                                                                  /cell_type="Sperm"
/note="Vector: pBeloBACll; Site_1: HindIII; Site_2:
HindIII"
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                                                                                                                                                                                                                                                                                                                                          Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                       /organism="Homo sapiens"
/db_xref="GDB:7148131"
                                                                                 /db_xref="taxon:9606"
/clone="2283N16"
/clone_lib="CIT-HSP"
/sex="Male"
Location/Qualifiers
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KEYWORDS
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prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostumi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
I (bases 1 to 165)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Haro.
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib "RIKEN full-length enriched, adult male medulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primed with a primer [5' GAGAGAGAAGAGGACCTTTTTTTTTTTTTVN 3'], CDNA was
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                          /note-"Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF881282 165 bp mRNA EST 17-JAN-20
QVI-ET0183-021200-529-d05_1 ET0183 Homo sapiens cbNA, mRNA
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                                                                                                                                                                                                               /tissue_type~"medulia oblongata"
/dev_stage~"adult"
/lab_host~"DH10B"
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/organism="Mus musculus"
                                                           /db_xref="taxon:10090"
/clone="6330552F17"
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12; Conservative
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                                                                                                                                                                                                                                                       /clone_lib_civ.v.
/dew_stage="Adult"
/dew_stage="Adult"
/note="Organ: lung_tumor; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
46 c 35 g 50 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 171)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deoliveira,P.E., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-ET0183-021200-529-d05_1&t3=2000-12-02&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 165.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be set in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=PM3&t2=PM3-UT0058-181000-007-g01&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 113.
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PM3-UT0058-181000-007-901 UT0058 Homo sapiens cDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/db_xref="taxon:9606"
/clone_lib="ET0183"
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source

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The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Liver library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1782730
                                                                                                                                                              /note="Organ: uterus_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A min!-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under the vector and vector an
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/lab_host="DH10B (Life Technologies)"
/lab_host="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-AI
and UI-R-E1 libraries. The UI-R-AI library consisted of a
mixture of individually tagged normalized libraries
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 172) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
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451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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UI-R-CO-iy-b-01-0-UI.s1 UI-R-CO Rattus norvegicus CDNA,clone
UI-R-CO-iy-b-01-0-UI 3', mRNA sequence.
AI029683.1 GI:4300245
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Program for Rat Gene Discovery and Mapping
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/db_xref="taxon:10116"
/clone="UI-R-C0-iy-b-01-0-UI"
/clone_lib="UI-R-C0"
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/db_xref="taxon:9606"
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                                                        /clone_lib-"UT0058"
                                                                                                                 /dev_stage="Adult"
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constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-Al and UI-R-EI clones from with the pooled UI-R-Al and UI-R-EI library in the form of single-stranded circles. The remaining single-stranded circles. The remaining single-stranded circles and electroporated to double-stranded circles and electroporated to bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described the bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
I (bases 1 to 173)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A2818519 173 bp DNA GSS 20-FEB-2001
2M0088A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0088A10 R, DNA sequence.
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Insert Length: 10000 Std Error: 0.00
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University of Utah
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Contact: Robert B. Weiss
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AZ818519.1 GI:12988427
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Best Local Similarity 100.
Matches 12; Conservative
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Fax: 801 585 7177
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COMMENT
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KEYWORDS
SOURCE
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TITLE

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/Jab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWP42nv; Purified genomic DNA from M.
musculus C57BL/5J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gil4732114]qblAR129072.1), a copy.number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Clones are derived from the mouse BAC library RPC1-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ985182 177 bp DNA GSS 30-JAN-2000 RPCI-23-307M5, TJ RPCI-23 Mus musculus genomic clone RPCI-23-307M5.
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Plate: 307 row: M column: 5
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Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 0200
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/db_xref="taxon:10090"
/clone="RPCI-23-307M5"
/clone=Llb="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain: Vector: pBACe3.6; Site_1:
FooRI: Site_2: EcoRI: Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
56 a 48 c 20 g 52 t lothers
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0; Gaps Query Match 100.0%; Score 12; DB 13; Length 177; Best Local Similarity 100.0%; Pred. No. 7e+03; Matches 12; Conservative 0; Mismatches 0; Indels (

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